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Date of mailing (day/month/year) 21 November 2000 (21.11.00)	
International application No. PCT/AU00/00385	Applicant's or agent's file reference 2288545/MRO
International filing date (day/month/year) 28 April 2000 (28.04.00)	Priority date (day/month/year) 29 April 1999 (29.04.99)
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1. The designated Office is hereby notified of its election made:

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/54, 15/11, 9/10, C12Q 1/48, 1/68, A01H 1/00, 5/00, C08B 3/02		A1	(11) International Publication Number: WO 00/66745 (43) International Publication Date: 9 November 2000 (09.11.00)
(21) International Application Number: PCT/AU00/00385 (22) International Filing Date: 28 April 2000 (28.04.00) (30) Priority Data: PQ0052/99 29 April 1999 (29.04.99) AU (71) Applicants (for all designated States except US): COMMON-WEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION [AU/AU]; Limestone Avenue, Campbell, Australian Capital Territory 2601 (AU). GOODMAN FIELDER LIMITED [AU/AU]; Level 42 Grosvenor Place, Sydney, New South Wales 2000 (AU). GROUPE LIMAGRAIN PACIFIC PTY LTD [AU/AU]; Level 31, 1 O'Connell Street, Sydney, New South Wales 2000 (AU). (72) Inventors; and (75) Inventors/Applicants (for US only): MORELL, Matthew [AU/AU]; 33 Wangara Street, Aranda, Australian Capital Territory 2614 (AU). LI, Zhongyi [AU/AU]; 63 Campaspe Circuit, Kaleen, Australian Capital Territory 2617 (AU). RAHMAN, Sadequr [AU/AU]; 46 Scarlett Street, Melba, Australian Capital Territory 2615 (AU). APPELS, Rudolph [AU/AU]; 40 Gingara Street, Aranda, Australian Capital Territory 2614 (AU).		(74) Agents: OLIVE, Mark, R. et al.; Davies Collison Cave, 1 Little Collins Street, Melbourne, Victoria 3000 (AU). (81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>	
(54) Title: NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES THEREFOR			
(57) Abstract <p>The present invention provides isolated nucleic acid molecules encoding wheat starch synthases, and probes and primers derived therefrom, which are useful in the modification of plant starch content and/or composition, and for screening plant lines to determine the presence of natural and/or induced mutations in starch synthase genes which affect starch content and/or composition. More particularly, the isolated nucleic acid molecules of the present invention further provide for the screening-assisted breeding of plants having desirable starch content and/or composition, in addition to providing for the direct genetic manipulation of plant starch content and/or composition.</p>			

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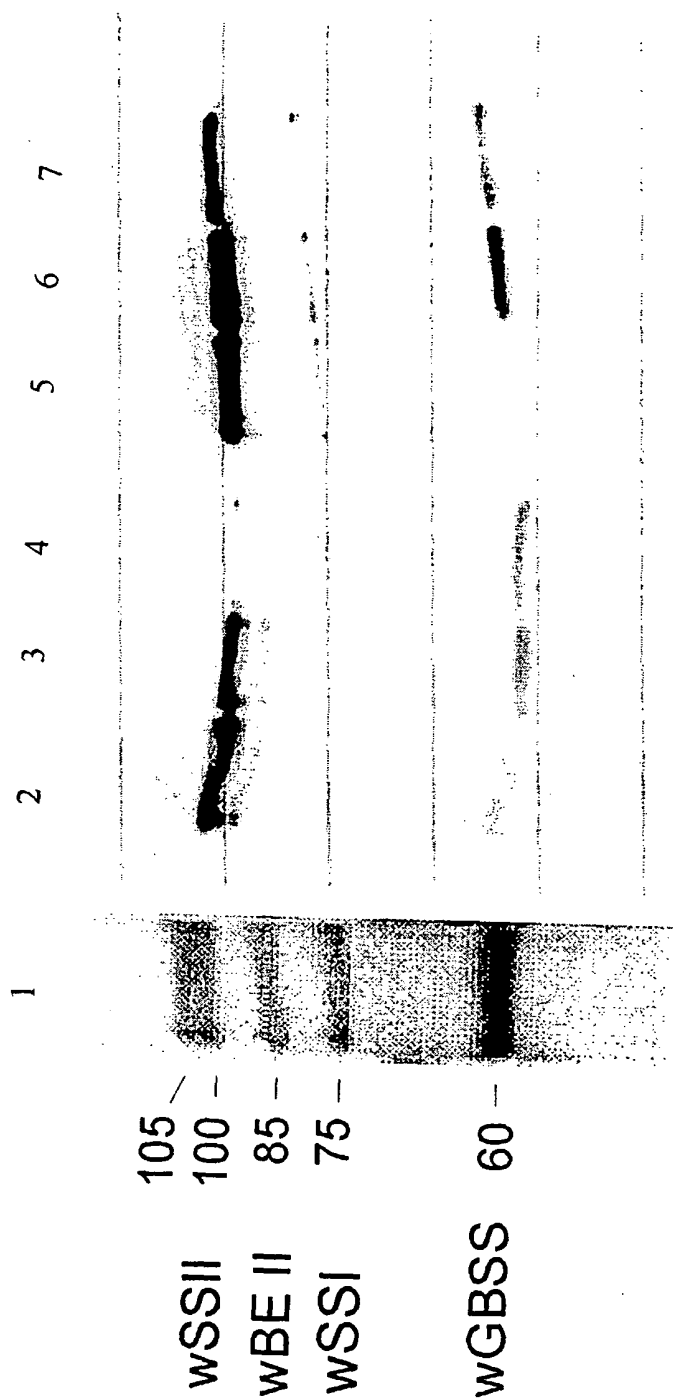


FIGURE 1

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FIGURE 2A
FIGURE 2B
FIGURE 2C
FIGURE 2D
FIGURE 2E
FIGURE 2F
FIGURE 2G
FIGURE 2H
FIGURE 2I
FIGURE 2J
FIGURE 2K
FIGURE 2L
FIGURE 2M
FIGURE 2N
FIGURE 2O

FIGURE 2

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1                                     50
wSSIIIB ATTTCTCTCGG CCTGACCCCG TGCGTTTACC CCACACAGAG CACACTCCAG
wSSIID ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

51                                     100
wSSIIIB TCCAGTCCAG CCCACTGCCG CGCTACTCCC CACTCCCACT GCCACCACT
wSSIID ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ GCT GCCACCACT

101                                    150
wSSIIIB CCGCCTGCCG CCGCTCTGG GCGGACCAAC CCGCGCATCG TATCACGATC
wSSIID ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA CCGCCTGCCG CCGCTCTGG GCGGAGGACC AACCCGCGCA TCGTACCATC

151                                    200
wSSIIIB ACCACCCCG ATCCCGGCCG CCGCCATGTC GTCGGCGGTC GCGTCCGCCG
wSSIID ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~
wSSIIA GCCCGCCCG ATCCCGGCCG CCGCCATGTC GTCGGCGGTC GCGTCCGCCG
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FIGURE 2A

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201          250
WSSIIB      CGTCCCTTCCT  CGCGCTCGCG  TCCGCCCTCCC  CCGGAGATC  ACGAGGAGG
WSSIID      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~
WSSIIA      CGTCCCTTCCT  CGCGCTCGCC  TCCGCCCTCCC  CCGGAGATC  ACGAGGCGG

251          300
WSSIIB      ACGAGGGTGA  GCGCGTCGCC  ACCCCACACC  GGGGCTGGCA  GGTGCACTG
WSSIID      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~
WSSIIA      GCGAGGGTGA  GCGCGCCGCC  ACCCCACGCC  GGGGCCGGCA  GGCTGCACTG

301          350
WSSIIB      GCCGCCGTCG  CCGCCGCAGC  GCACGGCTCG  CGACGGAGCG  GTGGCCGCGC
WSSIID      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~
WSSIIA      GCCGCCGTCG  CCGCCGCAGC  GCACGGCTCG  CGACGGAGGT  GTGGCCGCGC

351          400
WSSIIB      GCGCCGCCCG  GAAGAAGGAC  GCGGGGAT..  .CGACGACGC  CGCGCCCGCG
WSSIID      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~      ~~~~~~
WSSIIA      GCGCCGCCCG  GAAGAAGGAC  GCGAGGGTCG  ACGACGACGC  CGCGTCCGCG
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FIGURE 2B

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	401								450
wSSIIIB	AGGCAGCCCC	GCGCACTCCG	CGGTGGCGCC	GCCACCAAGG	TTGCGGAGCG				
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~				
wSSIIA	AGGCAGCCCC	GCGCACGCCG	CGGTGGCGCC	GcCACCAAGG	TCGCGGAGCG				
	451								500
wSSIIIB	GAGGGATCCC	GTCAAGACGC	TCGATCGCGA	CGCCGCGGAA	GGTGGCGCGC				
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~				
wSSIIA	GAGGGATCCC	GTCAAGACGC	TCGATCGCGA	CGCCGCGGAA	GGTGGCGCGC				
	501								550
wSSIIIB	CGTCCCCCGCC	GGCACCGAGG	CAGGAGGACG	CCCGTCTGCC	GAGCATGAAC				
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~				
wSSIIA	CGGCACCGCC	GGCACCGAGG	CAGGACGCCG	CCCGTCCaCC	GAGTATGAAC				
	551								600
wSSIIIB	GGCATGCCCGG	TGAACGGTGA	AAACAAATCT	ACCGCGGCGG	GCGGCGCGAC				
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~				
wSSIIA	GGCACGCCCGG	TGAACGGTGA	GAACAAATCT	ACCGCGGCGG	GCGGCGCGAC				

FIGURE 2C

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	601						650
wSSIIB	TAAAGACAGC	GGGCTGCCCG	CACCCGCACG	CGCGCCCCAG			CCGTCGAGCC
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~			~~~~~
wSSIIA	CAAAGACAGC	GGCTgcCCG	CACCCGcACG	CGCGCCCCAT			cCGTCGAcCC
	651						700
wSSIIB	AGAACAGAGT	ACCGGTGAAT	GGTGAAACA	AAGCTAACGT			CGCCTCGCCG
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~			~~~~~
wSSIIA	AgAACAgAGT	ACCAGTGAAC	GGTGAAACA	AAGCTAACGT			CGCCTCGCCG
	701						750
wSSIIB	CCGACGAGCA	TAGCCGAGGT	CGCGGCTCCG	GATCCCGCAG			CTACCATTC
wSSIID	~~~~~	~~~~~	~~~~~	~~~~~			~~~~~
wSSIIA	CCGACGAGCA	TAGCCGAGGT	CGTGGCTCCG	GATCCCGCAG			CTACCATTC
	751						800
wSSIIB	CATCAGTGAC	AAGCGCCAG	AGTCCGTTGT	CCCAGCCGAG			AAGCgcgcgc
wSSIID	~~~~~	~~~~~	~~~~~	~CCAGCTGAG			AAGACGCCGC
wSSIIA	CATCAGTGAC	AAGCGCCCG	AGTCCGTTGT	CCCAGCCGAG			AAGCCGCCGC

FIGURE 2D

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801      850
wSSIIIB CGtCgtcCgg CtcAAATtTc gtgCcCtCgg cttctGctCc cggGtctGAC
wSSIID  CGTCGTCCGG CTCAAATtTC GAGTCCtCGG CCTCTGCTCC CGGGTCTGAC
wSSIIA  CGTCGTCCGG CTCAAATtTC GTGgTCTCGG CTtCTGCTCC CAGGCTGGAC

851      900
wSSIIIB actgtCaGCG acGtGGaact TgaActGAag aAGGtgCgg tCattgTcaa
wSSIID  ACTGTCAGCG ACGTGAACA AGAACTGAAG AAGGTGCGG TCGTTGTCGA
wSSIIA  ATTGACAGCG ATGTTGAACC TGAActGAAG AAGGTGCGG TCATCGTCGA

901      950
wSSIIIB aGAAgcTcCa aaCcCaAaGG CTCTtTCGCC GCCCGCAGCA CCCGCTGTAC
wSSIID  AGAAGCTCCA AAGCCAAAGG CTCTtTCGCC GCctGCAGCc CCCGCTGTAC
wSSIIA  AGAAGCTCCA AACCCAAAGG CTCTtTCGCC GCCTGCAGCC CCCGCTGTAC

951      1000
wSSIIIB AACAAGACCT TTGGGACTTC AAGAAATACA TTGGtTTcGA GGAGCCCCGTG
wSSIID  AAgAAGACCT TTGGGAtTTC AAGAAATACA TTGGtTTcGA GGAGCCCCGTG
wSSIIA  AAGAAGACCT TTGGGACTTC AAGAAATACA TTGGCTTcGA GGAGCCCCGTG

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FIGURE 2E

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wSSIIB	1001	GAGGCCAAGG	ATGATGGCCG	GGCTGTTGCA	GATGATGCCG	GCTCCTTCGA	1050
wSSIID		GAGGCCAAGG	ATGATGGCCG	GGCTGTcGCA	GATGATGCCG	GCTCCTTtGA	
wSSIIA		GAGGCCAAGG	ATGATGGCTG	GGCTGTTGCA	GATGATGCCG	GCTCCTTTGA	
wSSIIB	1051	ACACCACCAG	AATCACGATT	CCGGGCCTTT	GGCAGGGGAG	AACGTCATGA	1100
wSSIID		ACACCACCAG	AATCACGACT	CCGGaCCTTT	GGCAGGGGAG	AAtGTCATGA	
wSSIIA		ACATCACCCAG	AACCATGATT	CCGGACCTTT	GGCAGGGGAG	AACGTCATGA	
wSSIIB	1101	ACGTGGTCGT	CGTGGCTGCT	GAATGTTCTC	CCTGGTGCAA	AACAGGTGGT	1150
wSSIID		ACGTGGTCGT	CGTGGCTGCT	GAgTGTtCTC	CCTGGTGCAA	AACAGGTGGT	
wSSIIA		ACGTGGTCGT	CGTGGCTGCT	GAATGTTCTC	CCTGGTGCAA	AACAGGTGGT	
wSSIIB	1151	CTTGGAGATG	TTGCCGGTGC	TTTGCCCAAG	GCTTTGGCGA	AGAGAGGACA	1200
wSSIID		CTgGGAGATG	TTGCgGGTGC	TcTGCCCAAG	GCTTTGGCaA	AGAGAGGACA	
wSSIIA		CTTGGAGATG	TTGCCGGTGC	TTTGCCCAAG	GCTTTGGCGA	AGAGAGGACA	

FIGURE 2F

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1201	1250
wSSII B	TCGTGTTATG GTTGTGGTAC CAAGGTATGG GGACTATGAG GAAGCCTACG
wSSII D	TCGTGTTATG GTTGTGGTAC CAAGGTATGG GGACTATGAa GAACCTACGg
wSSII A	TCGTGTTATG GTTGTGGTAC CAAGGTATGG GGACTATGAG GAAGCCTACG
1251	1300
wSSII B	ATGTCGGAGT CCGAAAATAC TACAAGGCTG CTGGACAGGA TATGGAAGTG
wSSII D	ATGTCGGAGT CCGAAAATAC TACAAGGCTG CTGGACAGGA TATGGAAGTG
wSSII A	ATGTCGGAGT CCGAAAATAC TACAAGGCTG CTGGACAGGA TATGGAAGTG
1301	1350
wSSII B	AATTATTTC ATGCTTATAT CGATGGAGTT GATTTTGTGT TCATTGACGC
wSSII D	AATTATTTC ATGCTTaTAT CGATGGAGTT GATTTTGTGT TCATTGACGC
wSSII A	AATTATTTC ATGCTTATAT CGATGGAGTT GATTTTGTGT TCATTGACGC
1351	1400
wSSII B	TCCTCTCTTC CGACACCGCC AGGAAGACAT TTATGGGGGC AGCAGACAGG
wSSII D	TCCTCTCTTC CGACACCGAG AGGAAGACAT TTATGGGGGC AGCAGACAGG
wSSII A	TCCTCTCTTC CGACACCGCC AGGAAGACAT TTATGGGGGC AGCAGACAGG

FIGURE 2G

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wSSIIIB	1401	AAATTATGAA	GCGCATGATT	TTGTTCTGCA	AGGCCGCTGT	CGAGGTTCCA	1450
wSSIID		AAATTATGAA	GCGCATGATT	TTGTTCTGCA	AGGCCGCTGT	TGAGGTTCCA	
wSSIIA		AAATTATGAA	GCGCATGATT	TTGTTCTGCA	AGGCCGCTGT	CGAGGTTCCCT	
wSSIIIB	1451	TGGCACGTTT	CATGCGGCGG	TGTCCCCTTAT	GGGGATGGAA	ATCTGGTGTT	1500
wSSIID		TGGCACGTTT	CATGCGGCGG	TGTCCCCTTAT	GGGGATGGAA	ATCTGGTGTT	
wSSIIA		TGGCACGTTT	CATGCGGCGG	TGTCCCCTTAT	GGGGATGGAA	ATCTGGTGTT	
wSSIIIB	1501	TATTGCAAAT	GATTGGCACA	CGGCACTCCT	GCCTGTCTAT	CTGAAAGCAT	1550
wSSIID		TATTGCAAAT	GATTGGCACA	CGGCACTCCT	GCCTGTCTAT	CTGAAAGCAT	
wSSIIA		TATTGCAAAT	GATTGGCACA	CGGCACTCCT	GCCTGTCTAT	CTGAAAGCAT	
wSSIIIB	1551	ATTACAGGGA	CCATGGTTTG	ATGCAGTACA	CTCGGTCCAT	TATGGTGATA	1600
wSSIID		ATTACAGGGA	CCATGGTTTG	ATGCAGTACA	CTCGGTCCAT	TATGGTGATA	
wSSIIA		ATTACAGGGA	CCATGGTTTG	ATGCAGTACA	CTCGGTCCAT	TATGGTGATA	

FIGURE 2H

	1601			1650
wSSII B	CATAACATCG	CTCACCAGGG	CCGTGGCCCCA	GTAGATGAGT
wSSII D	CATAACATCG	CTCACCAGGG	CCGTGGCCCT	GTAGATGAAT
wSSII A	CATAACATCG	CGCACCAGGG	CCGTGGCCCCA	GTAGATGAAT
				TCCCGTTCAC
				TCCCGTTCAC
				TCCCGTTCAC
	1651			1700
wSSII B	CGAGTTGCCT	GAGCACTACC	TGGAACACTT	CAGACTGTAC
wSSII D	CGAGTTGCCT	GAGCACTACC	TGGAACACTT	CAGACTGTAC
wSSII A	CGAGTTGCCT	GAGCACTACC	TGGAACACTT	CAGACTGTAC
				GACCCCGTGG
				GACCCCGTGG
				GACCCCGTGG
	1701			1750
wSSII B	GTGGTGAACA	CGCCAACTAC	TTCGCCGCCG	GCCTGAAGAT
wSSII D	GTGGTGAACA	CGCCAACTAC	TTCGCCGCCG	GCCTGAAGAT
wSSII A	GTGGTGAACA	CGCCAACTAC	TTCGCCGCCG	GCCTGAAGAT
				GCGGACCAG
				GCGGACCAG
				GCGGACCAG
	1751			1800
wSSII B	GTTGTCGTCG	TGAGCCCCGG	GTACCTGTGG	GAGCTGAAGA
wSSII D	GTTGTCGTCG	TGAGCCCCGG	GTACCTGTGG	GAGCTGAAGA
wSSII A	GTTGTCGTCG	TGAGCCCCGG	GTACCTGTGG	GAGCTCAAGA
				CGGTGGAGGG
				CGGTGGAGGG
				CGGTGGAGGG

FIGURE 2I

	2001					2050
wSSIIIB	TCCGCGGCGA	CGTGCCGCTG	CTCGGCTTCA	TCGGGCGCCT	GGACGGGCAG	
wSSIID	TCCGCGCCGA	CGTGCCGCTG	CTCGGCTTCA	TCGGGCGCCT	GGACGGGCAG	
wSSIIA	TCCGCGCCGA	CGTGCCGCTG	CTCGGCTTCA	TCGGGCGCCT	GGACGGGCAG	
	2051					2100
wSSIIIB	AAGGGCGTGG	AGATCATCGC	GGACGCCGATG	CCCTGGATCG	TGAGCCAGGA	
wSSIID	AAGGGCGTGG	AGATCATCGC	GGACGCCCATG	CCCTGGATCG	TGAGCCAGGA	
wSSIIA	AAGGGCGTGG	AGATCATCGC	GGACGCCCATG	CCCTGGATCG	TGAGCCAGgA	
	2101					2150
wSSIIIB	CGTGCAGCTG	GTGATGCTGG	GCACCGGGCG	CCACGACCTG	GAGGGCATGC	
wSSIID	CGTGCAGCTG	GTGATGCTGG	GCACCGGGCG	CCACGACCTG	GAGAGCATGC	
wSSIIA	CGTGCAGCTG	GTGATGCTGG	GCACCGGGCG	CCACGACcTG	gAGAGCATGC	
	2151					2200
wSSIIIB	TGCGGCACTT	CGAGCGGGAG	CACCACGACA	AGGTGCGCGG	GTGGGTGGGG	
wSSIID	TGAGCACTT	CGAGCGGGAG	CACCACGACA	AGGTGCGCGG	GTGGGTGGGG	
wSSIIA	TgCGGCACTT	CGAGCGGGAG	CACCACGACA	AGGTGCGCGG	gTGGGTGGGG	

FIGURE 2K

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2201	2250
wSSIIB TTCTCCGTGC GGCTGGCGCA CCGGATCACG GCCGGCGCCG ACGCGCTCCT	
wSSIID TTCTCCGTGC GCCTGGCGCA CCGGATCACG GCCGGCGCCG ACGCGCTCCT	
wSSIIA TTCTCCGTgc GccTGGCGCA CCGGATCACG GCCGGCGCCG ACGCGCTCct	
2251	2300
wSSIIB CATGCCCTCC CGGTTCGAGC CGTGCGGACT GAACCAGCTC TACGCCATGG	
wSSIID CATGCCCTCC CGGTTCGTGC CGTGCGGGCT GAACCAGCTC TACGCCATGG	
wSSIIA CATGCCCTCC CGGTTCGAgC CGTGCGGGTt GAACCAGCTt TACGCCATGG	
2301	2350
wSSIIB CCTACGGCAC CGTCCCCGTC GTGCATGCCG TCGGTGGCCT GAGGGACACC	
wSSIID CCTACGGCAC CGTCCCCGTC GTGCACGCCG TCGGCGGCCT CAGGGACACC	
wSSIIA CCTACGGCAC CGTCCCCGTC GTGCACGCCG TCGGCGGGGT GAGGGACACC	
2351	2400
wSSIIB GTGCCGCCGT TCGACCCCTT CAACCACTCC GGGCTCGGGT GGACGTTCGA	
wSSIID GTGCCGCCGT TCGACCCCTT CAACCACTCC GGGCTCGGGT GGACGTTCGA	
wSSIIA GTGCCGCCGT TCGACCCCTT CAACCACTCC GGcCTCGGGT GGACGTTCGA	

FIGURE 2L

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2401	2450
wSSIIB CCGCGCAGAG GCGCAGAAGC TGATCGAGGC GCTCGGGCAC TGCCTCCGCA	
wSSIID CCGCGCCGAG GCGCACAAGC TGATCGAGGC GCTCGGGCAC TGCCTCCGCA	
wSSIIA CCGGCGCGAG GCGCAcAAGC TGATCGAGGC GCTCGGGCAC TGCCTCCGCA	
2451	2500
wSSIIB CCTACCGGGA CTACAAGGAG AGCTGGAGGG GGCTCCAGGA GCGCGGCATG	
wSSIID CCTACCGGAG CTTCAAGGAG AGCTGGAGGG CCCTCCAGGA GCGCGGCATG	
wSSIIA CCTACCGGGA CTACAAGGAG AGCTGGAGGG GcCTCCAGGA GCGCGGCATG	
2501	2550
wSSIIB TCGCAGGACT TCAGCTGGGA GCATGCCGCC AAGCTCTACG AGGACGTCCT	
wSSIID TCGCAGGACT TCAGCTGGGA GCACGCCGCC AAGCTCTACG AGGACGTCCT	
wSSIIA TCGCAGGACT TCAGCTGGGA GCATGCCGCC AAGCTCTACG AGGACGTCCT	
2551	2600
wSSIIB CGTCAAGGCC AAGTACCAGT GGTGAACGCT AGCTGCTAGC CGGTCCAGCC	
wSSIID CGTCAAGGCC AAGTACCAGT GGTGAACGCT AGCTGCTAGC CGGTCCAGCC	
wSSIIA CcTCAAGGCC AAGTACCAGT GGTGAACGCT AGCTGCTAGC CgTCCAGCC	

FIGURE 2M

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2601                2650
WSSIIB      ...TGCATGA CAGGATGGAA TTGCGCATTTG CGCACGCAGG
WSSIID      ...TGCATGA CAGGATGGAA CT..GCATTG CGCACGCAGG
WSSIIA      GCATGcatgA gAGGgTGGAA cTGCGCATTTG CGCcCGCAGG

2651                2700
WSSIIB      AAGGTGCCAT ..... .GGAGCGCCG GCATCCGCCG AGTACAGTGA
WSSIID      AAAGTGCCAT ..... .GGAGCGCCG GCATCCGCCG AGTACAGTGA
WSSIIA      AACGTGCCAT ccttctcgat gGGAGCGCCG GCATCCGCCG gGTgCAGTGA

2701                2750
WSSIIB      CAT..GAGGT GTGTGTGGTT GAGACGCTGA TTC.....C GATCTGGTCC
WSSIID      CAT..GAGGT GTGTGTGGTT GAGACGCTGA TTC.....C AATCCGGCCC
WSSIIA      CATGAGagGT GTGTGTGGTT GAGACGCTGA TTCCGATCTc gatctGGTCC

2751                2800
WSSIIB      GTAGCAGAGT AGAGCGGAGG TAGGGAAGCG CTCCTTGTTA CAGGTATATG
WSSIID      GTAGCAGAGT AGAGCGGAGG TATATGGGAA TCTTAACCTG GTATTGTAAT
WSSIIA      GTAGCAGAGT AGAGCGGAcG TAGGGAAGCG CTCCTTGTTg CAGGTATATG
```

FIGURE 2N

	2801					2850
WSSIIB	GGAATGTTGT	TAACTTGGTA	TTGTAATTG	TTATGTTGTG	TGCATTATTA	
WSSIID	TTGTTATGTT	GTGTGCATTA	TTACAATGTT	GTTACTTATT	CTTGTTAAGT	
WSSIIA	GGAATGTTGT	CAACTTGGTA	TTGTAgtTTG	CTATGTTGTa	TGCgTTTATTA	
	2851					2900
WSSIIB	CAGAGGGCAA	CGATCTGCGC	CGGCGCACCG	GCCCAACTGT	TGGGCCCGGTC	
WSSIID	CGAGGGCCAA	GGCGAAAGC	TAGCTCACAT	GTCTGATGGA	TGCAAAAAAA	
WSSIIA	caatgttggt	acttattctt	gtTAAAAAAA	AAAAAaaaa	AAAA~~~~~	
	2901					2950
WSSIIB	GCACAGCAGC	CGTTGGATCC	GACCGCCTGG	GCCGTTGGAT	CCCACCGAAA	
WSSIID	AAAAAaaaa	AAA~~~~~	~~~~~	~~~~~	~~~~~	
WSSIIA	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
	2951	2965				
WSSIIB	AAAAAaaaa	AAAAA				
WSSIID	~~~~~	~~~~~				
WSSIIA	~~~~~	~~~~~				

FIGURE 20

FIGURE 3A
FIGURE 3B
FIGURE 3C
FIGURE 3D
FIGURE 3E
FIGURE 3F
FIGURE 3G

FIGURE 3

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WSSIIA	1	MSSAVASAAS	---	FLALASA	SP-GRSRRRA	RVSAPPPHAG	AGRL----	HW	PPWPP-QRTA	51
WSSIIB	1	*****	---	*****	***S***T*	***S***T*	***S***T*	***S***T*	***S***T*	51
WSSIID		-----	-----	-----	-----	-----	-----	-----	-----	
ZSSIIA	1	***AV*SS*	STF*****	***G***--	***GSS*F*T*	***S*SFAFWA	***S*SFAFWA	***S*SFAFWA	***S*SFAFWA	57
ZSSIIB	1	*PG*-I*SS*	SAFL*PV**S	***--R***G	S*G*ALRSY*	YSGAELRL**	ARRG*P*DG*	ARRG*P*DG*	ARRG*P*DG*	56
PEASSII	1	*MLSLG*D*T	VLP*H*KNLK	FTP*KL*TLNG	--DLAFSKGL	GVGRNLNCGSV	-----R	-----R	-----R	49
POTSSII	10	PVNFIFCDFY	VMENSI*LHS	GNQFHPNLPL	---LALRPKK	LSLIHGSSRE	-----Q	-----Q	-----Q	57

↓ Transit peptide cleavage site

WSSIIA.	52	RDGGVAARAA	GKKDARVDDD	AASARQPRAR	RGGAATKVAE	RRDPVKTLDR	DAAEGGAPAP	111
WSSIIB	52	***A*****	***GI--**	***p*****L	*****L	*****L	*****S*	110
WSSIID		-----	-----	-----	-----	-----	-----	
ZSSIIA	58	AALVR*EAE*	*G***PPERS	GDA**L***	*---NA*SK	***	-----	97
ZSSIIB	57	-ASVR**A*P	AGG-----	-----	-----	-----	-----	68
PEASSII	50	LNHKQHV**V	**SFGADENG	DG*EDDVVNA	TIEKSK**LA	LQRELIQQIA	ERKKLVSSID	109
POTSSII	58	MWRNQRVK*T	*ENSGEAA-S	*DESDALQV	TIEKSK**LA	MQQDLLQQIA	ERRKVVSSIK	116

FIGURE 3A

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WSSIIA	112	PAPRQDAARP	PSMNGTPVNG	ENKSTGGGGA	TKDSGLPAPA	RAPHPSTQNR	VPVNGENKAN	171
WSSIIB	111	*****ED**L	*****M****	*****	*****	***Q**S***	*****	170
WSSIID		-----	-----	-----	-----	-----	-----	
ZSSIIA	98	-----	-----	-----LQVPG	RYG*ATGNT*	*TGAA*C**A	ALADV*I*SI	132
ZSSIIB	69	-----	-----	-----	-ESEEAAKSS	SSSQAGAVQG	STAKAVDS*S	97
PEASSII	110	SDSIPGLEGN	GVSYESSEKS	LSR-----	-----	-----DS*P	QKGSSSSSGSA	146
POTSSII	117	S-----SL*NA	KGTYDGGSGS	LSDVDIPDVD	KDYNVTVPST	A*TGITDVK	NTPPAISHDF	172
WSSIIA	172	VASPPTSIAE	VVAPDSAATI	SISDKAPESV	VPAEKPPPPSS	GSNFVVSASA	PRLDIDSDVE	231
WSSIIB	171	*****	*A***p****	*****	*****A****	*****P****	*GS*TV****	230
WSSIID	203	-----	-----	-----	*****T****	*****ES****	*GS*TV****	231
ZSSIIA	134	*A***VK	FP**GYRMIL	PSG*I**T*	L**P**--LH	E*PA*DGD*N	--GIAPPT**	188
ZSSIIB	99	PPN*L**APK	QSQAAMQNG	TSGGSSASTA	A*VSG*KADH	P*AP*TKREI	DASAVKPEPA	158
PEASSII	147	*ETKR--WHC	FQQ-----LC	RSKETETWA*	SSVGINQGF	EIEKKND*VK	ASSKLHFNEQ	199
POTSSII	173	*E*KREIKRD	LADERAPPLS	RS*IT*SSQI	SSTVSSK--R	TL*VPPETPK	SSQETLL**N	230

FIGURE 3B

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Sgp-1 Peptide 3									
WSSIIA	350	RYGDYEEAYD	VGVRKYYKAA	GQDMEVNYFH	AYIDGVDFVF	IDAPLFRHRQ	EDIYGGSRQE	409	
WSSIIB	349	*****	*****	*****	*****	*****	*****	408	
WSSIID	350	*****PT*	*****	*****	*****	*****E	*****	409	
ZSSIIA	283	***V**F*	**I*****	**L*****	*F*****	*****	D*****	342	
ZSSIIB	249	***E**R*	L***RR**V*	***S**T***	S*****	VE**P***H	NN***E*LD	308	
PEASSII	303	H**N*A**H*	I***R**V*	***T***	T*****I**	**S*I**NLE	SN*****LD	362	
POTSSII	338	*DN*P*PQ*	S***I**VD	**VD*T**Q	*LLMDC****	*HSHM***IG	NN*****N*VD	397	
Region 3									
WSSIIA	410	IMKRMILFCK	AAVEVPWHVP	CGGVPYGDGN	LVFIANDWHT	ALLPVYLKAY	YRDHGLMQYT	469	
WSSIIB	409	*****	*****	*****	*****	*****	*****	468	
WSSIID	410	*****	*****	*****	*****	*****	*****	469	
ZSSIIA	343	*****	V*****	***C*****	*****	*****	*****	402	
ZSSIIB	309	*L*****	*****YA*	**TV*****	*****	*****	*****A	368	
PEASSII	363	*LR**V****	*****	**IC*****	*****	*****	*****N**	422	
POTSSII	398	*L***V****	**I*****	***C*****	*****	***A*****	***N*I*N**	457	

FIGURE 3D

```

WSSIIA 470 RSIMVIHNIA HQGRGPVDEF PFTELPEHYL EHFRLYDPVG GEHANYFAAG LKMADQVVVV 529
WSSIIB 469 ***** ***** ***** ***** ***** ***** ***** 528
WSSIID 470 ***** ***** ***** ***** ***** ***** ***** 529
ZSSIIA 404 **VL***** **YMD***** Q**E***** *****I***** *****R**T* 462
ZSSIIB 369 **VL***** **VNFD*****I D**K*****NI* *D*S*V***** **T**R**T* 428
PEASSII 423 **VL***** **NTVD*SGN** DL*KM***** **F*I***** **T**R**T* 482
POTSSII 458 **VL***** **SYVD**P**M DP*K***** **F*I***** **T**R**T* 517

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Region 4

```

WSSIIA 530 SPGYLWELKT VEGGWGLHDI IRQNDWKTRG IVNGIDNMEW NPEVDVHLK- SDGYTNFSLG 588
WSSIIB 529 ***** ***** ***** ***** ***** ***** ***** 587
WSSIID 530 ***** ***** ***** ***** ***** A*****R 588
ZSSIIA 463 *R*****IN* *****HQ** *K*****R- *****Y**E 521
ZSSIIB 429 *N**M***** S*****LQ* *****MS** *A*****H- *****YTFE 487
PEASSII 483 *H**A***** S*****N* *NES***F** *****V*TKD* **QF*AY*T- *****YN*K 541
POTSSII 518 *H**S***** SQ*****Q* *NE*****LQ* *****TK** ***L*****PR *****M*Y**D 577

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FIGURE 3E

Region 5										Region 5a									
WSSIIA	589	TLDGKRQCK	EALQRELGLQ	VRADVPLLGF	IGRLDGQKGV	EIIADAMPWI	VSQDVQLVML												648
WSSIIB	588	*****	*****	**G*****	*****	*****	*****												647
WSSIID	588	*****	*****	*****	*****	*****	*****												648
ZSSIIA	522	**A*****	A*****E	**D*****	*****	D**G*****	AG*****												581
ZSSIIB	488	**T*****	A**Q*****	**D**I**	*****H*****	D*****IH**	AG*****												547
PEASSII	542	**QT*****	A*****P	**E**IIS*	*****H*****	DL**E*I**M	M**H*****												601
POTSSII	578	**QT**P**	A**K****P	**D****I**	*****P*****	DL**E*V**M	MG*****												637
Region 6																			
WSSIIA	649	GTGRHDLESM	LRHFEREHHD	KVRGWVGFVS	RLAHRITAGA	DALLMPSRFE	PCGLNQLYAM												708
WSSIIB	648	*****G*	*****	*****	*****	*****	*****												707
WSSIID	649	*****	*Q*****	*****	*****	*****	*****												708
ZSSIIA	582	***A***R*	*Q*L*****PN	*****	PM*****	*V*****	*****												641
ZSSIIB	548	***A***D*	**R**S**S*	**A*****	P*****	*I*****	*****												607
PEASSII	602	***A***Q*	*KE**AQ*C*	*I*S*****	KM*****	*I*****	*****												661
POTSSII	638	***R***Q*	**Q**CQ*N*	*I*****	KTS*****	*I*****	**A*****												697

FIGURE 3F

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		Region 7									
WSSIIA	709	AYGTVPVVHA	VGGVRDTPPP	FDPFNHSGLG	WTFDRAEAHK	LIEALGHCLR	TYRDYKESWR	768			
WSSIIB	708	*****	***L****	*****	*****Q*	*****	*****	767			
WSSIID	709	*****	***L****	*****	*****	*****	***F*****	768			
ZSSIIA	642	*****	***L****A*	***GDA**	*****N*	***R****D	***K*G***K	701			
ZSSIIB	608	*****	***L****A*	***DT***	*****NR	M*D**S***T	***N*****	667			
PEASSII	662	S*****G	***L****Q*	*N**DE**V*	*****N*	*MA**WN**L	**K***K**E	721			
POTSSII	698	K***I*****	***L****Q*	***LMSQDW*	GPS*****SQ	**PRIRN**L	***E**K**E	757			
WSSIIA	769	GLQERGMSQD	FSWEHAAKLY	EDVLLKAKYQ	W	799					
WSSIIB	768	*****	*****	***V*****	*	798					
WSSIID	769	*****	*****	***V*****	*	799					
ZSSIIA	702	S**A*****	L**D***E**	***V*****	*	732					
ZSSIIB	668	ACRA***AE*	L**D***V**	***V*****	*	698					
PEASSII	722	*I*****	L**DN**QQ*	*E**VA*****	*	752					
POTSSII	759	*I*T*C*T**	L**DN**QN*	*E**IA*****	*	788					

FIGURE 3G

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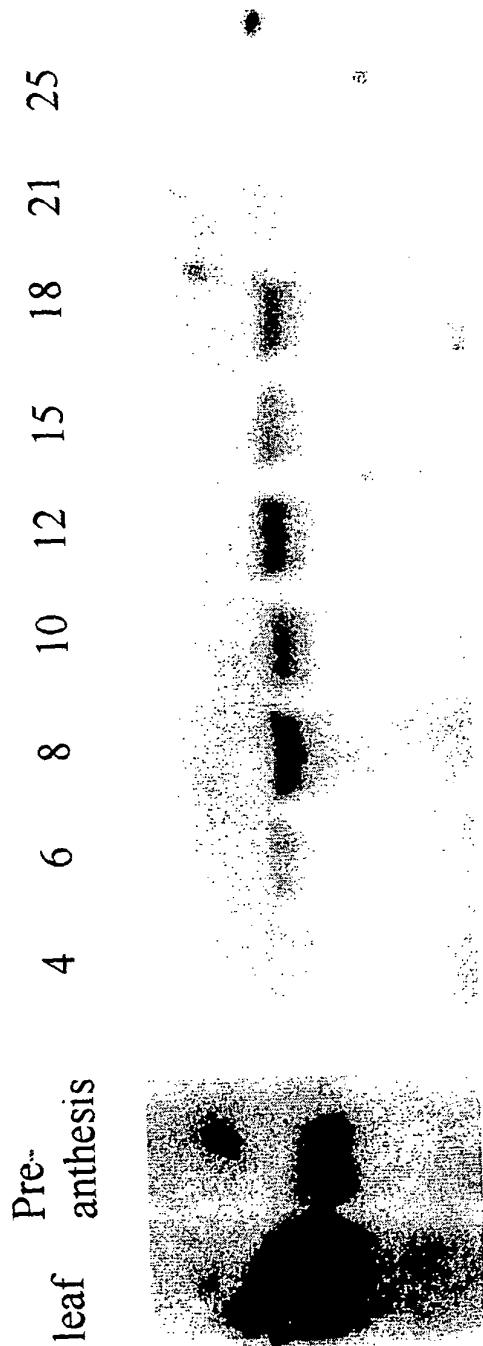


FIGURE 4

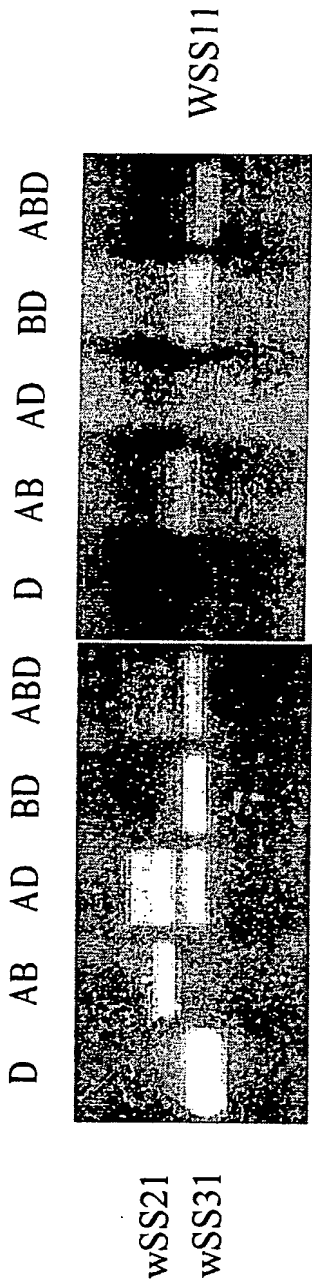


FIGURE 5

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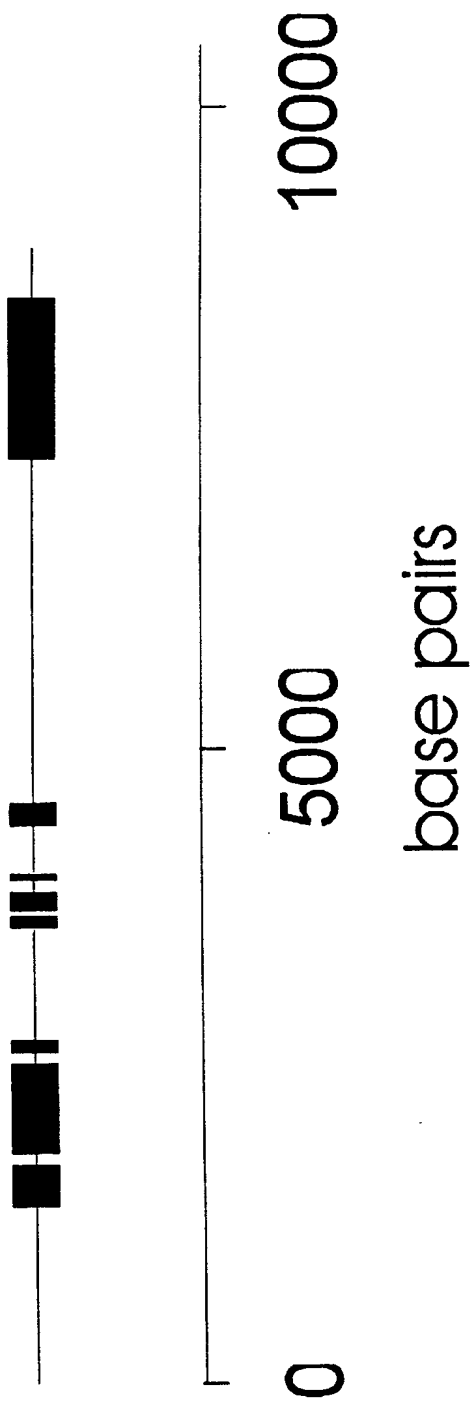


FIGURE 6

FIGURE 7A
FIGURE 7B
FIGURE 7C
FIGURE 7D
FIGURE 7E
FIGURE 7F
FIGURE 7G
FIGURE 7H
FIGURE 7I

FIGURE 7

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1      MEMSLWPRSP LCPRSRQPLV VVRP..AGRG GLTQPFMLNG RFTRSRTRLRC      50
wSSIII
mSSIII MEMVLRSPSP LCLRS.GPVL IFRPTVAGGG GGTQSLRLTT RFARRRVIRC
pSSIII ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

51     MVASSDPPNR KRRMVPPQV KVISSRGYTT RLIVEPSNEN TEHNNRD...      100
wSSIII
mSSIII VVASPGCPNR KS.RTASPNV KVAAYSNYAP RLLVESSKK SEHHDSSRHR
pSSIII ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

101    EETLDTYNAL LSTETAETD NREAE..... ..TAKADSSQ NALSSSIIGE      150
wSSIII
mSSIII EETIDTYNGL SGSDAAELTS NRDVEIEVDL QHISEEELPG KVSINASLGE
pSSIII ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

151    VDVAD..... EDILAADLTV YSLSSVMKKE VDAADKARVK EDAFELDLP      200
wSSIII
mSSIII METVDEAEVE EDKFEVDTSI IVLRNVAVRE VDPKDEHNAK .DVFVVDSSG
pSSIII ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

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FIGURE 7A

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401          450
wSSIII ADQDTFEADL SGNASSCATY REVDDVVDET RSEETTFAMD LFAESGHEK
mSSIII VSSHGQDKSI VG.VPQQIQY NDQSIAGSHR QDQSIAGAPE QIQSVAGYIK
pSSIII ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~MDVPPF

451          500
wSSIII HMAVDYVGEA TDEETYQQQ YVPSSFMSW DKAIKTGVS LNPELRLLVRV
mSSIII PNQ.SIVGSC KQHELIPEP KKIESIISYN EIDQSIVGSH KQDKSVVSV
pSSIII PLHRSLSCTS VSNAITHLKI KPILGFVSHG TTSLSVQSSS WRKDGMMVTGV

501          550
wSSIII EEQGVNFSD KKDLSIDDL P GQNQSIIGSY KQDKSIADVA GPTQSI FGSS
mSSIII EQIQSIVSHS KPNQSTVDSY RQAESIIGVP EKVQSITSYD KLDQSI VGS
pSSIII SFSICANFSG RRRRKVSTPR SQGSSPKGFV PRKPSGMSTQ RKVQKSNGDK

551          600
wSSIII KQHR SIVAFP KQNQ SIVSVT EQKQ SIVGFR SQDLSAVSL. ....P
mSSIII KQDEPIISVP EKIQ SIVHYT KPNQ SIVGLP KQQQ SIVHIV EPKQSIDGFP
pSSIII ESKSTSTSKE SEISNQKTVE ARVETSDDDT KGVVRDHKFL EDEDEINGST

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FIGURE 7C

33/50

601				650	
wSSIII	KQ.NVPIVGT	SREGQTKQVP	VVDRQDALYV	NGLEAKEGDH	TSEKTD DAL
mSSIII	KQ.DLSIVGI	SNEFQTKQLA	TVGTHDGLLM	KGVEAKE...	TSQKTEGDTL
pSSIII	KSISMSPPRV	SSQFVESEET	GGDDKDAVKL	N..KSKRSEE	SGFIIDSVIR
651				700	
wSSIII	HVKFNVDNVL	RKHQADRTQA	VEKKTWKKVD	EEHLYMTEHQ	KRAA..EGQM
mSSIII	QATFNVDNLS	QKQEGLTKEA	DEITIEKIN	DEDLVMIEEQ	KSIAMNEEQT
pSSIII	EQSGSQGETN	ASSKGSHAVG	TKLYEILQVD	VEPQQQLKEN.	.NAGNVEYKKG
701				750	
wSSIII	VVNEDELSIT	EIGMGRGD.K	IQHVLSEEL	SWSEDEVQLI	EDDGQYEVDE
mSSIII	IVTEEDIPMA	KVEIGIDKAK	FLHLLSEES	SWDENEVGII	EAD EQYEVDE
pSSIII	PVASKLLEIT	KA.....SD	VEHTESNEID	DLDTN..SFF	KSDLIEE DEP
751				800	
wSSIII	TSVSVNVEQD	IQGSPQDVVD	PQALKVMLQE	LAEKNYSMRN	KLFVFPPEVVK
mSSIII	TSMS..TEQD	IQESPNDDDL	PQALWSMLQE	LAEKNYSLGN	KLFTYDPDLK
pSSIII	LAAGTVETGD	SSLNLRLEME	ANLRRQAIER	LAEENLLQGI	RLFCFPPEVVK

FIGURE 7D

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801					850
wSSIII	ADSVIDLVLN	RDLTALANEP	DVVIKGAENG	WKWRLFTERL	HKSDLGGVWW
mSSIII	ADSTIDLVLN	RDLTALANEP	DVLIKGAENG	WKWRLFTERL	HKSELAGDWW
pSSIII	PDEDVEIFLN	RGLSTLKNES	DVLIMGAFNE	WYRSFTTTRL	TETHLNGDWW
851					900
wSSIII	SCKLYIPKEA	YRLDFVFFNG	RTVYENNGNN	DFCIGIEGTM	NEDLFEDFLV
mSSIII	CCKLYIPKQA	YRMDVFFNG	HTVYENNNNN	DFVIQIESTM	DENLFEDFLA
pSSIII	SCKIHVPKEA	YRADFVFFNG	QDVYDNNDGN	DFSITVKGGM	QIIDFENFLL
901					950
wSSIII	KEKQRELEKL	AMEEAERRTQ	TEEQRRRKEA	RAADEAVRAQ	AKAEIEIKKK
mSSIII	EEKQRELENL	ANEEAERRRQ	TDEQRRMEEE	RAADKADRVQ	AKVEVETKKN
pSSIII	EEKWREQEKL	AKEQAERERL	AEEQRRIEAE	KAEIEADRAQ	AKEEAAKKKK
951					1000
wSSIII	KLQSMLSLAR	TCVDNLWYIE	ASTDTRGDTI	RLYNNRNSRP	LAHSTEIWMH
mSSIII	KLCNVLGLAR	APVDNLWYIE	PITGQEATV	RLYNNRNSRP	LHSTEIWMH
pSSIII	VLRELMVKAT	KTRDITWYIE	PSEFKCEDKV	RLYNNKSSGP	LSHAKDLWIH

FIGURE 7E

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	1001		1050
wSSIII	GGYNNWTDGL	SIVESFVKCN	DKDGDWWYAD
mSSIII	GGYNNWIDGL	SFAERLVHHH	DKDCDWWFAD
pSSIII	GGYNNWKDGL	SIVKKLVKSE	RIDGDWWYTE
			VVIPDQALFL
			DWVFADGPPK
	1051		1100
wSSIII	NARNYDNNAR	QDFHAILPNN	NVTEEGFWAQ
mSSIII	SARNYDNNGG	HDFHATLP.N	NMTTEEYWME
pSSIII	HAIAYDNNHR	QDFHAIVP.N	HIPEELYWVE
			EEHQIFKTLQ
			EERRLREAAAM
	1101		1150
wSSIII	KRKAERSANI	KAEMKAKTMR	RFLSQKHIV
mSSIII	KRKAERNAKM	KAEMKEKTMR	MFLVSQKHIV
pSSIII	RAKVEKTALL	KTETKERTMK	SFLSQKHVV
			YTEPLDIQAG
			SSVTVYYNPA
	1151		1200
wSSIII	NTVLNGKSEG	WFRCSFNLWM	HSSGALPPQK
mSSIII	NTVLTGKPEV	WFRCSFNRWM	YPGGVLPPQK
pSSIII	NTVLNGKPEI	WFRCSFNRWT	HRLGPLPPQK
			MSPAENGTHV
			RATVKVPLDA

FIGURE 7F

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	1201		1250
wSSIII	YMMDFVFSEW	EEDGIYDNRN	GMDYHIPVSD SIETENYMRI IHIAVEMAPV
mSSIII	YMMDFVFSES	EEGGIYDNRN	GLDYHIPVFG SIAKEPPMHI VHIAVEMAPI
pSSIII	YMMDFVFSEW	EDGGIFDNKS	GMDYHIPVFG GVAKEPPMHI VHIAVEMAPI
	1251		1300
wSSIII	AKVGGLGDVV	TSLSRAIQDL	GHTVEVILPK YDCLNQSSVK DLHLYQSFSW
mSSIII	AKVGGLGDVV	TSLSRAVQDL	GHNVEVILPK YGCLNLSNVK NLQIHQSFSW
pSSIII	AKVGGLGDVV	TSLSRAVQDL	NHNVDIILPK YDCLKMNNVK DFRFHKNYFW
	1301		1350
wSSIII	GGTEIKVWVG	RVEDLTVYFL	EPQNGMFGVG CVYG.RNDDR RFGFFCHSAL
mSSIII	GGSEINVWRG	LVEGLCVYFL	EPQNGMFGVG YVYG.RDDDR RFGFFCRSAL
pSSIII	GGTEIKVWFG	KVEGLSVYFL	EPQNGLFSKG CVYGCSNDGE RFGFFCHAAL
	1351		1400
wSSIII	EFILQNEFSP	HHCHDWSS	APVAWLKHEH YSQSRMASTR VVFTIHNLEF
mSSIII	EFLQSGSSP	NIIHCHDWSS	APVAWLHKEN YAKSSLANAR VVFTIHNLEF
pSSIII	EFLQGGFSP	DIHCHDWSS	APVAWLFEQ YTHYGLSKSR IVFTIHNLEF

FIGURE 7G

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1401					1450
wSSIII	GAHYIGKAMT	YCDKATTVSP	TYSRDVAGHG	AIAPHREKFY	GILNGIDPDI
mSSIII	GAHHIGKAMR	YCDKATTVSN	TYSKEVSGHG	AIVPHLGKFY	GILNGIDPDI
pSSIII	GADLIGRAMT	NADKATTVSP	TYSQEVSGNP	VIAPHLHKFH	GIVNGIDPDI
1451					1500
wSSIII	WDPYTDNFIP	VPYTCENVVE	GKRAAKRALQ	QKFGLQQTDV	PIVGIIITRLT
mSSIII	WDPYNDNFIP	VHYTCENVVE	GKRAAKRALQ	QKFGLQQIDV	PVVGIVITRLT
pSSIII	WDPLNDKFIP	IPYTSENVVE	GKTAAKEALQ	RKLGLKQADL	PLVGIIITRLT
1501					1550
wSSIII	AQKGIHLIKH	AIHRTLESNG	HVVLLGSAPD	HRIQGDFCRL	ADALHGVYHG
mSSIII	AQKGIHLIKH	AIHRTLERNG	QVVLLGSAPD	SRIQADFVNL	ANTLHGVNHG
pSSIII	HQKGIHLIKH	AIWRTLERNG	QVVLLGSAPD	PRVQNNFVNL	ANQLHSKYND
1551					1600
wSSIII	RVKLVLTIDE	PLSHLIYAGS	DFIIVPSIFE	PCGLTQLVAM	RYGSIPIVRK
mSSIII	QVRLSLTYDE	PLSHLIYAGS	DFILVPSIFE	PCGLTQLVAM	RYGTIPIVRK
pSSIII	RARLCLTYDE	PLSHLIYAGA	DFILVPSIFE	PCGLTQLTAM	RYGSIPVVRK

FIGURE 7H

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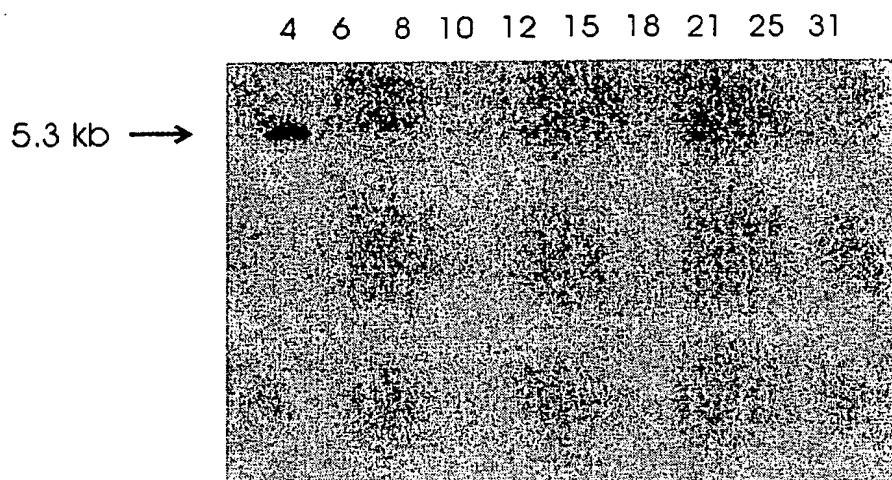
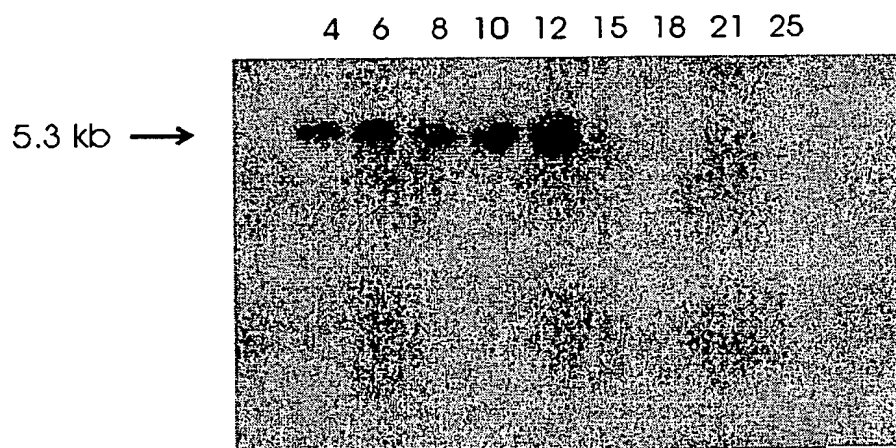
[a] Wyuna**[b] Gabo****[c] Gabo****FIGURE 8**

FIGURE 9A	FIGURE 9B
FIGURE 9C	FIGURE 9D
FIGURE 9E	FIGURE 9F

FIGURE 9

Region 1				Region 2			
10				20			
				30			
				40			
				50			
wGBSS	81	FVGAEMAPWS	KTGGLGDLG	GLPPAMAANG	HRVMVISPRY	DQYKDAWDT-	
wSS1	144	-*TG*A**YA	*S*****VC*	S*I*L**R*	*****VM***	LNGSSDKNYA	
wSS2	314	--A**CS**C	*****VA*	A**K*L*KR*	*****VV***	GD*EE*Y*V-	
wSS3	1187	-IAV****VA	*V*****VVT	S*SR*IQDL*	*T*E**L*K*	*CLNQSSVK-	
100				110			
				120			
				130			
				140			
wGBSS	171	LEKVRGKTKE	KIYGPDAGTD	YEDNQRFSL	LCQAALVPR	ILNLDNNPYF	
wSS1	234	-HRPGSLYGD	-----NFGA	FG***F*YT*	**Y**C*A*L	**E*GGYI*G	
wSS2	404	RHRQEDIYGG	-----S	RQEIMK*MI*	F*K**V***W	HVPCGGV**G	
wSS3	1277	*PQN*MFGV	-----GCVY	GRNDDR**GF	F*HS***--F	**QNEFS*H-	
190				200			
				210			
				220			
				230			
wGBSS	261	FCIHNISYQG	RFSFDDEAQL	NLPD-----R	FKSSFDFIDG	YDKPVEGRKI	
wSS1	324	LV***LAH**	LEPASTYPD*	G**PEWYGAL	EWVFPEWARR	HALDKGEAVN	
wSS2	494	MV*****AH**	*GPV*E*PFT	E*-----	-EHYLEHFRL	**PVGGEHAN	
wSS3	1367	*T***L-EF*	AHYIGKAMTY	CDK-----	-----	-----	

FIGURE 9A

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60	70	80	90	
-----SVVSE	IKVVDK YERV	RYFHCYKRGV	DRVFDHPCF	170
KALYTGKHIK	*PCFGGSHE*	TF**E*RDN*	*W*****SY	233
-----G*RKY	Y*AAGQDME*	N***A>ID**	*F**I*A*L*	403
-----	-DLHLYQSFS	WGGTEI*VW*	G**EDLTVY*	1276
Region 3				
150	160	170	180	
SGPYGEDVVF	VCNDWHTGLL	ACYLKSNYQS	NGIYRAAKVA	260
QN-----CM*	*V***AS*V	PVL*AAK*RP	Y*V**DSRST	323
D*-----NL**	IA*****A**	PV***AY*RD	H*LMQYTRSI	493
-----II	H*H**SSAPV	*WLY*EH*SQ	-SRMASTR*V	1366
240	250	260	270	
NWMKAGILQA	DKVLTVSPYY	AELISGEAR	GCELDNIMRL	350
FLKG*VVTAD	RI*TVSQG*S	W*VTTAEGGQ	*LNELLSS*K	413
YFAAGLKMAD	QV*VVSPG*L	W*LKTVEGGW	*LHDIIRQND	583
-----	-----AT	TVSPTYSRDV	AGHGAIAPHR	1456

FIGURE 9B

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		Region 4				
		280	290	300	310	320
wGBSS	351	TGITTIVNGM	DVSEWDPTKD	KFLAVNYDIT	TALEGKALNK	EALEGKALNK
wSS1	414	SVLNG***I	*IND*N**T*	*C*PHH*SV-	-----	DD*S**KC*
wSS2	584	WKTRG***I	*NM**N*EV*	VH*KSDGYTN	-----FSLG	TLDS**RQC*
wSS3	1457	EKFYG*L*I	*PDI***YT*	N*IP*P*TCE	-----NVVEG*	**AKRALQQ*

		Region 5a				
		370	380	390	400	410
wGBSS	441	LKEEDVQIVL	LGTGKKKFER	LLKSIEEKFP	SKVRAVVRFN	-----APLA
wSS1	504	*MR***F*M	**S*DPI**G	WMR*T*SSYK	D*F*GW*G*S	-----V*VS
wSS2	674	V-SQ***L*M	****RHDL*S	M*RHF*REHH	D**GW*G*S	-----VR**
wSS3	1547	TL*SNG*V**	**SAPDHRIQ	GDFCRLADAL	HG*YHGRVKL	-VLTUDE**S

FIGURE 9C

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Region 5			
330	340	350	360
EALQAEVGLP	VDRKVPLVAF	IGRLEEQKGP	DVMIASIPEI 440
AE**K*L**	*RED**IG*	***DY***I	*LIKMA*** 503
R*L**Q	*RADLG*	***DG***V	EIIADAM*W* 673
FG**QT----	---D**I*GI	*T***TA***I	-HL*KHAIHR 1546

Region 6				Region 7	
420	430	440	450		
HQMMAGADVL	AVTSRFEPCG	LIQLQGMRYG	TPCACASTGG	530	
*RIT**C*I*	LMP*****	*N**YA*Q**	*VPVVG***	593	
*RIT***A*	LMP*****	*N**YA*A**	*VPVHVAV**	763	
*LIY**S*FI	I*P*I*****	*T***VA***	SIPIVRK***	1636	

FIGURE 9D

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Region 7 (Continued)

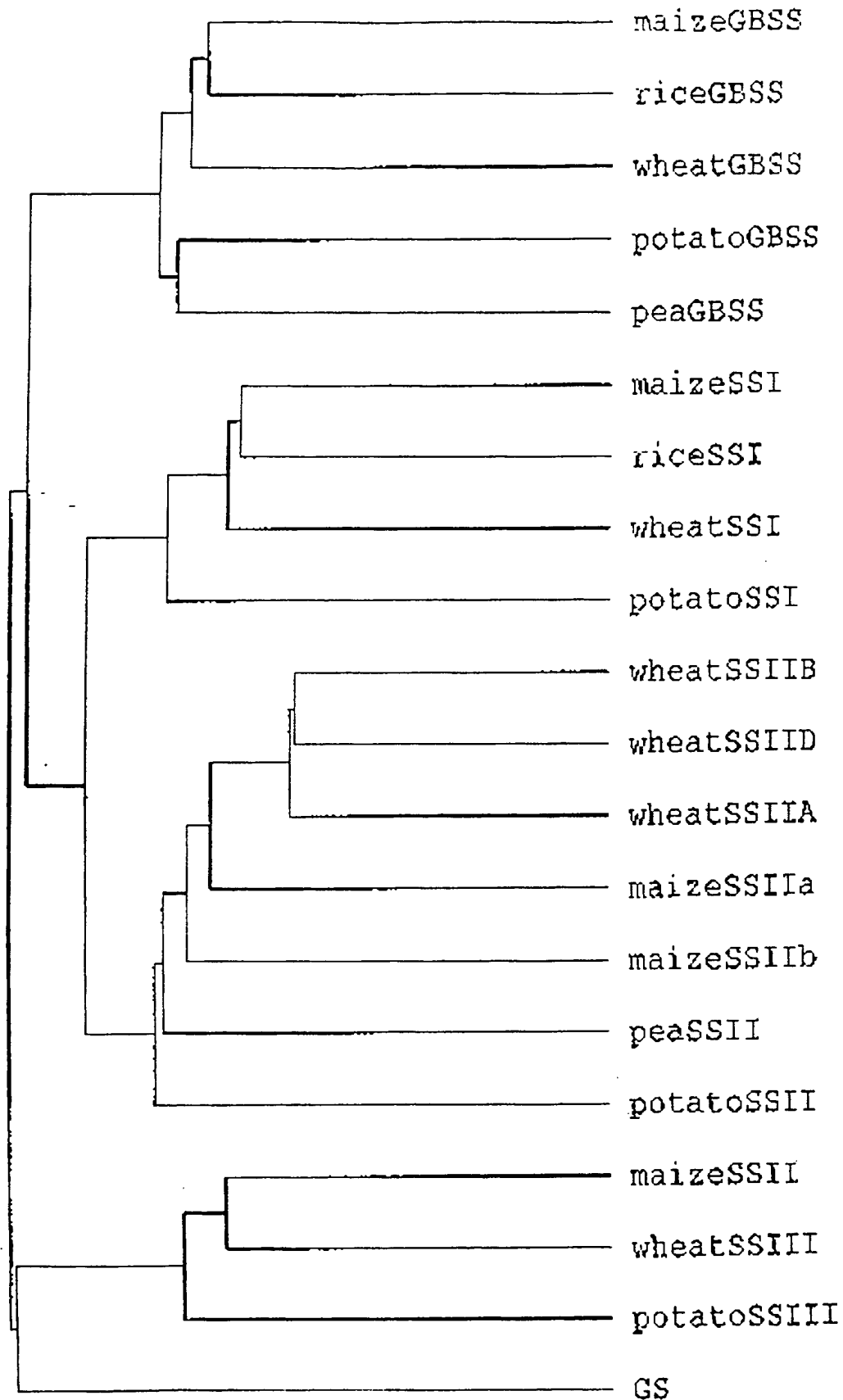
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wSS1 594	*R**--**TFN	-----	--PFGAKGEE	GTGWAFSPLT	VDKMLW*LRT
wSS2 764	VR**--*PPFD	-----	--PFNHSGLG	---W*FD**E	AHKLIE*LGH
wSS3 1637	***--*FDV	NDKDRAR*LG	LEPNGFSFDG	ADSNVGVDY*L	NRAIGAWFDA
550	560	570	580	590	600
wGBSS 621	APLAMENVAA	P*
wSS1 684	FVDQPYVM..
wSS2 854	KYQW.....
wSS3 1727

FIGURE 9E

510	520	530	540	
MVKNCMIQDL	SWKGPKNWE	DVLELGVGE	SEPGIVGEEI	620
AMSTFEHKE	**E*LM*RGM	TKDHTWDHAA	EQYEQIF*WA	683
CLRTYRDYKE	**R*LQERGM	SQDFSWEHAA	KLYED*LLKA	853
RDWFHSLCKK	VMEQDWSWNR	PA*DYIELYH	AARKE*....	1726
610	620	630		
.....	710
.....	773
.....	943
.....	1816

FIGURE 9F

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**FIGURE 10**

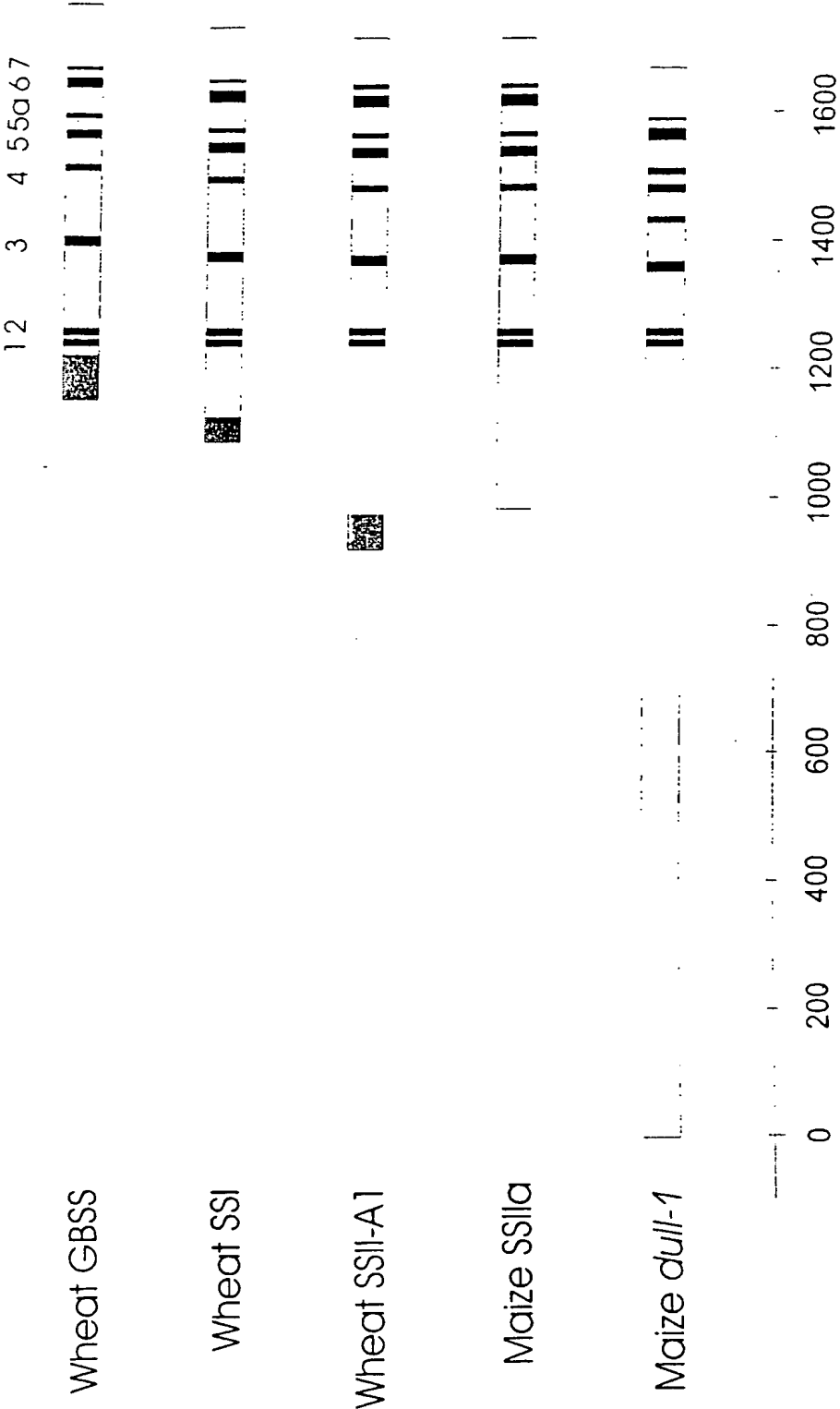


FIGURE 11

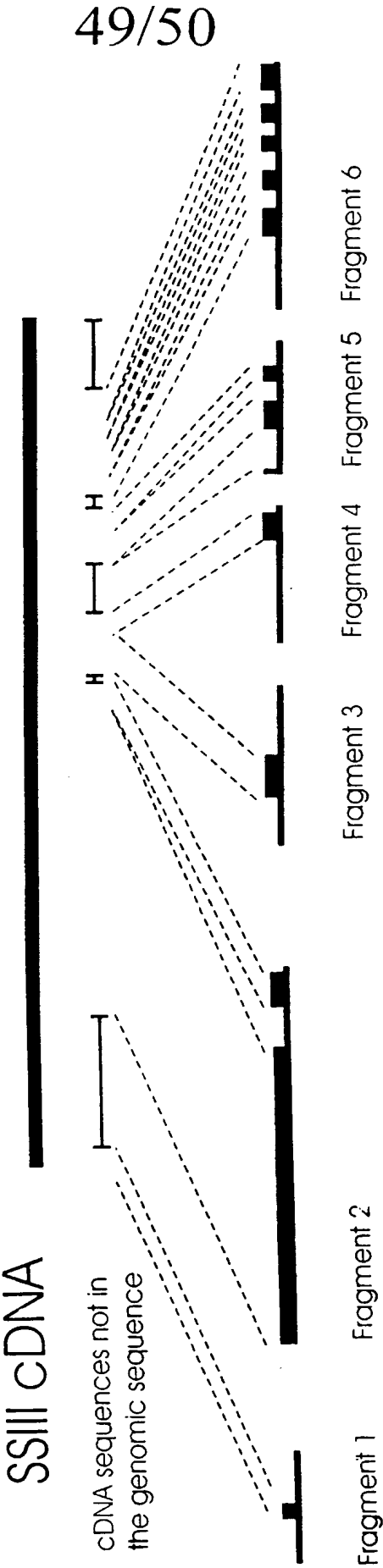


FIGURE 12

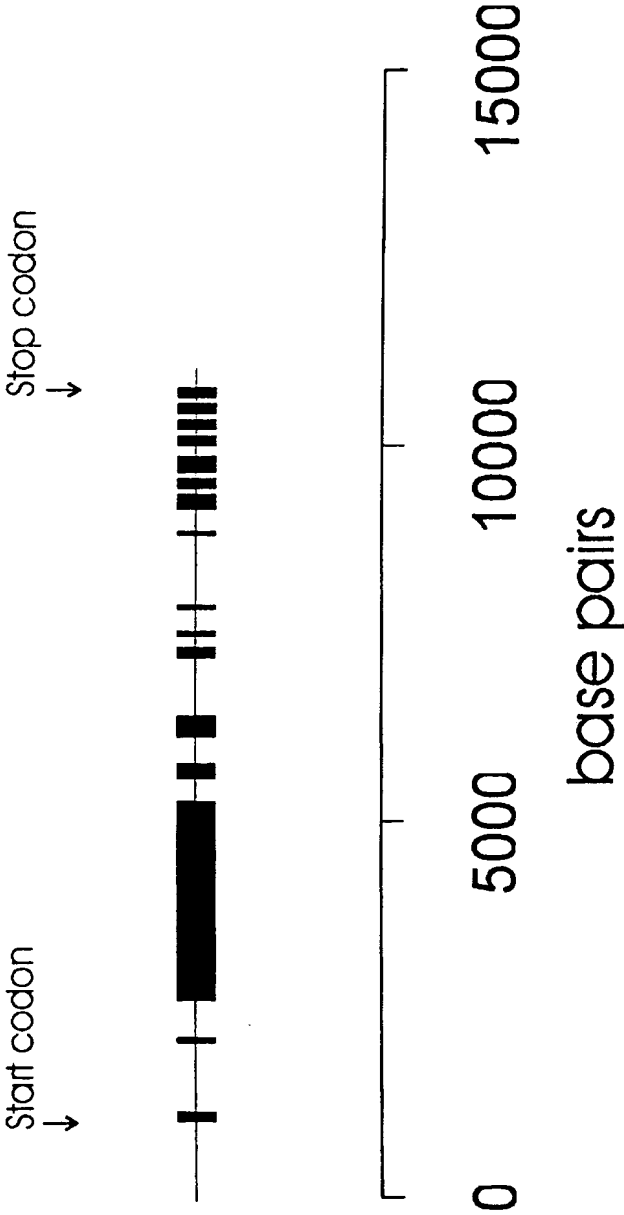


FIGURE 13

- 1 -

SEQUENCE LISTING

<110> COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
GOODMAN FIELDER LIMITED
GROUPE LIMAGRAIN PACIFIC PTY LTD

<120> NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES
THEREFOR

<130> p:\oper\mro\pi-wss.pct

<140> TO BE ADVISED

<141> 2000-04-28

<150> AU PQ0052/99

<151> 1999-04-29

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gcggaaccaac ccgcgcacgc tatcacgac acccaccgcc atcccgggcc cgcgc atg 178
                                         Met
                                         1

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tcc ccc ggg aga tca cgg agg agg acg agg gtg agc gcg tcg cca ccc 274
Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro Pro
          20              25              30

cac acc ggg gct ggc agg ttg cac tgg ccg ccg tcg ccg ccg cag cgc 322
His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln Arg
          35              40              45

acg gct cgc gac gga gcg gtg gcc gcg cgc gcc gcc ggg aag aag gac 370
Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys Asp
          50              55              60              65

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Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Pro Arg Ala Leu Arg
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Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys Thr
          85              90              95

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- 2 -

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Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu Asp Ile	
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Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu Phe Cys	
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Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly Leu Met	
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Gln Tyr Thr Arg Ser Ile Met Val Ile His Asn Ile Ala His Gln Gly	
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Arg Gly Pro Val Asp Glu Phe Pro Phe Thr Glu Leu Pro Glu His Tyr	
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Val	Gly	Phe	Ser	Val	Arg	Leu	Ala	His	Arg	Ile	Thr	Ala	Gly	Ala	Asp
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Ala	Leu	Leu	Met	Pro	Ser	Arg	Phe	Glu	Pro	Cys	Gly	Leu	Asn	Gln	Leu
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Glu Leu Lys Lys Gly Ala Val Ile Val Glu Glu Ala Pro Asn Pro Lys				
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250 255 260				
ttc aag aaa tac att ggc ttc gag gag ccc gtg gag gcc aag gat gat	928			
Phe Lys Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp				
265 270 275 280				
ggc tgg gct gtt gca gat gat gcg ggc tcc ttt gaa cat cac cag aac	976			
Gly Trp Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn				
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Val Ala Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp				
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Val Ala Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val				
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Met Val Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Ala Tyr Asp Val				
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Gly Val Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn				
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tat ttc cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct	1264			
Tyr Phe His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala				
380 385 390				

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Pro Leu Phe Arg His Arg Gln Glu Asp Ile Tyr Gly Gly Ser Arg Gln	
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gaa att atg aag cgc atg att ttg ttc tgc aag gcc gct gtc gag gtt	1360
Glu Ile Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val	
410 415 420	
cct tgg cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg	1408
Pro Trp His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu	
425 430 435 440	
gtg ttt att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg	1456
Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu	
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aaa gca tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att	1504
Lys Ala Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile	
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atg gtg ata cat aac atc gcg cac cag ggc cgt ggc cca gta gat gaa	1552
Met Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu	
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Phe Pro Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu	
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Tyr Asp Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu	
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Lys Met Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu	
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ctc aag acg gtg gag ggc ggc tgg ggg ctt cac gac atc ata cgg cag	1744
Leu Lys Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln	
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Asn Asp Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu	
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Trp Asn Pro Glu Val Asp Val His Leu Lys Ser Asp Gly Tyr Thr Asn	
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Phe Ser Leu Gly Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala	
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Leu Gln Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu	
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Gly Phe Ile Gly Arg Leu Asp Gly Gln Lys Gly Val Glu Ile Ile Ala	
620 625 630	
gac gcc atg ccc tgg atc gtg agc cag gac gtg cag ctg gtc atg ctg	2032
Asp Ala Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu	
635 640 645	

- 10 -

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 Gly Thr Gly Arg His Asp Leu Glu Ser Met Leu Arg His Phe Glu Arg
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 Glu His His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu
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 Ala His Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg
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 Val Pro Val Val His Ala Val Gly Gly Val Arg Asp Thr Val Pro Pro
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gag gcg cac aag ctg atc gag gcg ctc ggg cac tgc ctc cgc acc tac 2368
 Glu Ala His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr
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cgg gac tac aag gag agc tgg agg ggc ctc cag gag cgc ggc atg tcg 2416
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 Gln Asp Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu
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 Leu Lys Ala Lys Tyr Gln Trp
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 Arg Thr Ala Arg Asp Gly Gly Val Ala Ala Arg Ala Ala Gly Lys Lys
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 Asp Ala Arg Val Asp Asp Asp Ala Ala Ser Ala Arg Gln Pro Arg Ala
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 Arg Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val
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 Lys Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ala Pro Pro
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 Ala Pro Arg Gln Asp Ala Ala Arg Pro Pro Ser Met Asn Gly Thr Pro
 115 120 125
 Val Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp
 130 135 140
 Ser Gly Leu Pro Ala Pro Ala Arg Ala Pro His Pro Ser Thr Gln Asn
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 Arg Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro
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 Thr Ser Ile Ala Glu Val Val Ala Pro Asp Ser Ala Ala Thr Ile Ser
 180 185 190
 Ile Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Pro Pro
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 Pro Ser Ser Gly Ser Asn Phe Val Val Ser Ala Ser Ala Pro Arg Leu
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 Asp Ile Asp Ser Asp Val Glu Pro Glu Leu Lys Lys Gly Ala Val Ile
 225 230 235 240
 Val Glu Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro
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 Ala Val Gln Glu Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu
 260 265 270
 Glu Pro Val Glu Ala Lys Asp Asp Gly Trp Ala Val Ala Asp Asp Ala
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 Gly Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly
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 Glu Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp
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 Cys Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala
 325 330 335
 Leu Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly
 340 345 350
 Asp Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala
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 Ala Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly
 370 375 380

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Val Asp Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu
 385 390 395 400
 Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu
 405 410 415
 Phe Cys Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly
 420 425 430
 Val Pro Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His
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 Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly
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 Leu Met Gln Tyr Thr Arg Ser Ile Met Val Ile His Asn Ile Ala His
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 485 490 495
 His Tyr Leu Glu His Phe Arg Leu Tyr Asp Pro Val Gly Gly Glu His
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 Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met Ala Asp Gln Val Val Val
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 Val Asn Gly Ile Asp Asn Met Glu Trp Asn Pro Glu Val Asp Val His
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 Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln Arg Glu Leu Gly Leu Gln
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 Val Arg Ala Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp Gly
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 Gln Lys Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser
 625 630 635 640
 Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu
 645 650 655
 Ser Met Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly
 660 665 670
 Trp Val Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala
 675 680 685
 Asp Ala Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln
 690 695 700
 Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly
 705 710 715 720
 Gly Val Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly

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Leu Gly His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg			
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Ala Ser Ala Pro Gly Ser Asp Thr Val Ser Asp Val Glu Gln Glu Leu			
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aag aag ggt gcg gtc gtt gtc gaa gaa gct cca aag cca aag gct ctt			144
Lys Lys Gly Ala Val Val Val Glu Glu Ala Pro Lys Pro Lys Ala Leu			
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tcg ccg cct gca gcc ccc gct gta caa gaa gac ctt tgg gat ttc aag			192
Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp Phe Lys			
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aaa tac att ggt ttc gag gag ccc gtg gag gcc aag gat gat ggc cgg			240
Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp Gly Arg			
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gct gtc gca gat gat gcg ggc tcc ttt gaa cac cac cag aat cac gac			288
Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn His Asp			
85	90	95	
tcc gga cct ttg gca ggg gag aat gtc atg aac gtg gtc gtc gtg gct			336
Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val Val Ala			
100	105	110	
gct gag tgt tct ccc tgg tgc aaa aca ggt ggt ctg gga gat gtt gcg			384
Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Ala			
115	120	125	
ggt gct ctg ccc aag gct ttg gca aag aga gga cat cgt gtt atg gtt			432
Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val Met Val			
130	135	140	
gtg gta cca agg tat ggg gac tat gaa gaa cct acg gat gtc gga gtc			480
Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Pro Thr Asp Val Gly Val			
145	150	155	160

- 14 -

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Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe	
165 170 175	
cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct cct ctc	576
His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu	
180 185 190	
ttc cga cac cga gag gaa gac att tat ggg ggc agc aga cag gaa att	624
Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile	
195 200 205	
atg aag cgc atg att ttg ttc tgc aag gcc gct gtt gag gtt cca tgg	672
Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp	
210 215 220	
cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg gtg ttt	720
His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe	
225 230 235 240	
att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg aaa gca	768
Ile Ala Asn Asp Trp His Thr Ala Leu Pro Val Tyr Leu Lys Ala	
245 250 255	
tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att atg gtg	816
Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val	
260 265 270	
ata cat aac atc gct cac cag ggc cgt ggc cct gta gat gaa ttc ccg	864
Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro	
275 280 285	
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Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp	
290 295 300	
ccc gtg ggt ggt gaa cac gcc aac tac ttc gcc gcc ggc ctg aag atg	960
Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met	
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gcg gac cag gtt gtc gtg gtg agc ccc ggg tac ctg tgg gag ctg aag	1008
Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys	
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acg gtg gag ggc ggc tgg ggg ctt cac gac atc ata cgg cag aac gac	1056
Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln Asn Asp	
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Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu Trp Asn	
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ccc gag gtg gac gcc cac ctc aag tcg gac ggc tac acc aac ttc tcc	1152
Pro Glu Val Asp Ala His Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser	
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Leu Arg Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln	
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cgc gag ctg ggc ctg cag gtc cgc gcc gac gtg ccg ctg ctc ggc ttc	1248
Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu Gly Phe	
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- 15 -

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atg ccc tgg atc gtg agc cag gac gtg cag ctg gtg atg ctg ggc acc 1344
Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu Gly Thr
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ggg cgc cac gac ctg gag agc atg ctg cag cac ttc gag cgg gag cac 1392
Gly Arg His Asp Leu Glu Ser Met Leu Gln His Phe Glu Arg Glu His
      450      455      460

cac gac aag gtg cgc ggg tgg gtg ggg ttc tcc gtg cgc ctg gcg cac 1440
His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu Ala His
      465      470      475      480

cgg atc acg gcg ggg gcg gac gcg ctc ctc atg ccc tcc cgg ttc gtg 1488
Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg Phe Val
      485      490      495

ccg tgc ggg ctg aac cag ctc tac gcc atg gcc tac ggc acc gtc ccc 1536
Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro
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gtc gtg cac gcc gtc ggc ggc ctc agg gac acc gtg ccg ccg ttc gac 1584
Val Val His Ala Val Gly Gly Leu Arg Asp Thr Val Pro Pro Phe Asp
      515      520      525

ccc ttc aac cac tcc ggg ctc ggg tgg acg ttc gac cgc gcc gag gcg 1632
Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala
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cac aag ctg atc gag gcg ctc ggg cac tgc ctc cgc acc tac cga gac 1680
His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr Arg Asp
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ttc aag gag agc tgg agg gcc ctc cag gag cgc ggc atg tcg cag gac 1728
Phe Lys Glu Ser Trp Arg Ala Leu Gln Glu Arg Gly Met Ser Gln Asp
      565      570      575

ttc agc tgg gag cac gcc gcc aag ctc tac gag gac gtc ctc gtc aag 1776
Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu Val Lys
      580      585      590

gcc aag tac cag tgg tgaacgctag ctgctagccg ctccagcccc gcatgcgtgc 1831
Ala Lys Tyr Gln Trp
      595

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aagtacagtg acatgaggtg tgtgtggttg agacgctgat tccaatccgg cccgtagcag 1951

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Lys Lys Gly Ala Val Val Val Glu Glu Ala Pro Lys Pro Lys Ala Leu	35	40	45
Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp Phe Lys	50	55	60
Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp Gly Arg	65	70	75
Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn His Asp	85	90	95
Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val Val Ala	100	105	110
Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Ala	115	120	125
Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val Met Val	130	135	140
Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Pro Thr Asp Val Gly Val	145	150	155
Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe	165	170	175
His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu	180	185	190
Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile	195	200	205
Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp	210	215	220
His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe	225	230	235
Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala	245	250	255
Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val	260	265	270
Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro	275	280	285
Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp	290	295	300
Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met	305	310	315
Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys	325	330	335
Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln Asn Asp	340	345	350

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 Pro Glu Val Asp Ala His Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser
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 Leu Arg Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln
 385 390 395 400
 Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu Gly Phe
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 420 425 430
 Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu Gly Thr
 435 440 445
 Gly Arg His Asp Leu Glu Ser Met Leu Gln His Phe Glu Arg Glu His
 450 455 460
 His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu Ala His
 465 470 475 480
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 485 490 495
 Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro
 500 505 510
 Val Val His Ala Val Gly Gly Leu Arg Asp Thr Val Pro Pro Phe Asp
 515 520 525
 Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala
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 His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr Arg Asp
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 Phe Lys Glu Ser Trp Arg Ala Leu Gln Glu Arg Gly Met Ser Gln Asp
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 Ser Pro Leu Cys Pro Arg Ser Arg Gln Pro Leu Val Val Val Arg Pro

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act cga agc agg acc ctt cga tgc atg gta gca agt tca gat cct cct Thr Arg Ser Arg Thr Leu Arg Cys Met Val Ala Ser Ser Asp Pro Pro 45 50 55			196
aat agg aaa tca aga agg atg gta cca cct cag gtt aaa gtc att tct Asn Arg Lys Ser Arg Arg Met Val Pro Pro Gln Val Lys Val Ile Ser 60 65 70			244
tct aga gga tat acg aca aga ctc att gtt gaa cca agc aac gag aat Ser Arg Gly Tyr Thr Thr Arg Leu Ile Val Glu Pro Ser Asn Glu Asn 75 80 85			292
aca gaa cac aat aat cgg gat gaa gaa act ctt gat aca tac aat gcg Thr Glu His Asn Asn Arg Asp Glu Glu Thr Leu Asp Thr Tyr Asn Ala 90 95 100			340
cta tta agt acc gag aca gca gaa tgg aca gat aat aga gaa gcc gag Leu Leu Ser Thr Glu Thr Ala Glu Trp Thr Asp Asn Arg Glu Ala Glu 105 110 115 120			388
act gct aaa gcg gac tcg tcg caa aat gct tta agc agt tct ata att Thr Ala Lys Ala Asp Ser Ser Gln Asn Ala Leu Ser Ser Ser Ile Ile 125 130 135			436
ggg gaa gtg gat gtg gcg gat gaa gat ata ctt gcg gct gat ctg aca Gly Glu Val Asp Val Ala Asp Glu Asp Ile Leu Ala Ala Asp Leu Thr 140 145 150			484
gtg tat tca ttg agc agt gta atg aag aag gaa gtg gat gca gcg gac Val Tyr Ser Leu Ser Ser Val Met Lys Lys Glu Val Asp Ala Ala Asp 155 160 165			532
aaa gct aga gtt aaa gaa gac gca ttt gag ctg gat ttg cca gca act Lys Ala Arg Val Lys Glu Asp Ala Phe Glu Leu Asp Leu Pro Ala Thr 170 175 180			580
aca ttg aga agt gtg ata gta gat gtg atg gat cat aat ggg act gta Thr Leu Arg Ser Val Ile Val Asp Val Met Asp His Asn Gly Thr Val 185 190 195 200			628
caa gag aca ttg aga agt gtg ata gta gat gtg atg gat cat aat ggg Gln Glu Thr Leu Arg Ser Val Ile Val Asp Val Met Asp His Asn Gly 205 210 215			676
act gta caa gag aca ttg aga agt gtg ata gta gat gtg atg gat gat Thr Val Gln Glu Thr Leu Arg Ser Val Ile Val Asp Val Met Asp Asp 220 225 230			724
gcg gcg gac aaa gct aga gtt gaa gaa gac gta ttt gag ctg gat ttg Ala Ala Asp Lys Ala Arg Val Glu Glu Asp Val Phe Glu Leu Asp Leu 235 240 245			772
tca gga aat att tca agc agt gcg acg acc gtg gaa cta gat gcg gtt Ser Gly Asn Ile Ser Ser Ser Ala Thr Thr Val Glu Leu Asp Ala Val 250 255 260			820
gac gaa gtc ggg cct gtt caa gac aaa ttt gag gcg acc tca tca gga Asp Glu Val Gly Pro Val Gln Asp Lys Phe Glu Ala Thr Ser Ser Gly 265 270 275 280			868

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aat gtt tca aac agt gca acg gta cgg gaa gtg gat gca agt gat gaa	916
Asn Val Ser Asn Ser Ala Thr Val Arg Glu Val Asp Ala Ser Asp Glu	
285 290 295	
gct ggg aat gat caa ggc ata ttt aga gca gat ttg tca gga aat gtt	964
Ala Gly Asn Asp Gln Gly Ile Phe Arg Ala Asp Leu Ser Gly Asn Val	
300 305 310	
ttt tca agc agt aca aca gtg gaa gtg ggt gca gtg gat gaa gct ggg	1012
Phe Ser Ser Ser Thr Thr Val Glu Val Gly Ala Val Asp Glu Ala Gly	
315 320 325	
tct ata aag gac agg ttt gag acg gat tcg tca gga aat gtt tca aca	1060
Ser Ile Lys Asp Arg Phe Glu Thr Asp Ser Ser Gly Asn Val Ser Thr	
330 335 340	
agt gcg ccg atg tgg gat gca att gat gaa acc gtg gct gat caa gac	1108
Ser Ala Pro Met Trp Asp Ala Ile Asp Glu Thr Val Ala Asp Gln Asp	
345 350 355 360	
aca ttt gag gcg gat ttg tcg gga aat gct tca agc tgc gca aca tac	1156
Thr Phe Glu Ala Asp Leu Ser Gly Asn Ala Ser Ser Cys Ala Thr Tyr	
365 370 375	
aga gaa gtg gat gat gtg gtg gat gaa act aga tca gaa gag gaa aca	1204
Arg Glu Val Asp Asp Val Val Asp Glu Thr Arg Ser Glu Glu Thr	
380 385 390	
ttt gca atg gat ttg ttt gca agt gaa tca ggc cat gag aaa cat atg	1252
Phe Ala Met Asp Leu Phe Ala Ser Glu Ser Gly His Glu Lys His Met	
395 400 405	
gca gtg gat tat gtg ggt gaa gct acc gat gaa gaa gag act tac caa	1300
Ala Val Asp Tyr Val Gly Glu Ala Thr Asp Glu Glu Glu Thr Tyr Gln	
410 415 420	
cag caa tat cca gta ccg tct tca ttc tct atg tgg gac aag gct att	1348
Gln Gln Tyr Pro Val Pro Ser Ser Phe Ser Met Trp Asp Lys Ala Ile	
425 430 435 440	
gct aaa aca ggt gta agt ttg aat cct gag ctg cga ctt gtc agg gtt	1396
Ala Lys Thr Gly Val Ser Leu Asn Pro Glu Leu Arg Leu Val Arg Val	
445 450 455	
gaa gaa caa ggc aaa gta aat ttt agt gat aaa aaa gac ctg tca att	1444
Glu Glu Gln Gly Lys Val Asn Phe Ser Asp Lys Lys Asp Leu Ser Ile	
460 465 470	
gat gat tta cca gga caa aac caa tcg atc att ggt tcc tat aaa caa	1492
Asp Asp Leu Pro Gly Gln Asn Gln Ser Ile Ile Gly Ser Tyr Lys Gln	
475 480 485	
gat aaa tca att gct gat gtt gcg gga ccg acc caa tca att ttt ggt	1540
Asp Lys Ser Ile Ala Asp Val Ala Gly Pro Thr Gln Ser Ile Phe Gly	
490 495 500	
tct agt aaa caa cac ccg tca att gtt gct ttc ccc aaa caa aac cag	1588
Ser Ser Lys Gln His Arg Ser Ile Val Ala Phe Pro Lys Gln Asn Gln	
505 510 515 520	
tca att gtt agt gtc act gag caa aag cag tcc ata gtt gga ttc cgt	1636
Ser Ile Val Ser Val Thr Glu Gln Lys Gln Ser Ile Val Gly Phe Arg	
525 530 535	

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agt caa gat ctt tcg gct gtt agt ctc cct aaa caa aac gta cca att	1684
Ser Gln Asp Leu Ser Ala Val Ser Leu Pro Lys Gln Asn Val Pro Ile	
540 545 550	
ggt ggt acg tcg aga gag ggt caa aca aag caa gtt cct gtt gtt gat	1732
Val Gly Thr Ser Arg Glu Gly Gln Thr Lys Gln Val Pro Val Val Asp	
555 560 565	
aga cag gat gca ttg tat gtg aat gga ctg gaa gct aag gag gga gat	1780
Arg Gln Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp	
570 575 580	
cac aca tcc gag aaa act gat gag gat gcg ctt cat gta aag ttt aat	1828
His Thr Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn	
585 590 595 600	
ggt gac aat gtg ttg cgg aag cat cag gca gat aga acc caa gca gtg	1876
Val Asp Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val	
605 610 615	
gaa aag aaa act tgg aag aaa gtt gat gag gaa cat ctt tac atg act	1924
Glu Lys Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr	
620 625 630	
gaa cat cag aaa cgt gct gcc gaa gga cag atg gta gtt aac gag gat	1972
Glu His Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp	
635 640 645	
gag ctt tct ata act gaa att gga atg ggg aga ggt gat aaa att cag	2020
Glu Leu Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln	
650 655 660	
cat gtg ctt tct gag gaa gag ctt tca tgg tct gaa gat gaa gtg cag	2068
His Val Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln	
665 670 675 680	
tta att gag gat gat gga caa tat gaa gtt gac gag acc tct gtg tcc	2116
Leu Ile Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser	
685 690 695	
ggt aac gtt gaa caa gat atc cag ggg tca cca cag gat gtt gtg gat	2164
Val Asn Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp	
700 705 710	
ccg caa gca cta aag gtg atg ctg caa gaa ctc gct gag aaa aat tat	2212
Pro Gln Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr	
715 720 725	
tcg atg agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat	2260
Ser Met Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp	
730 735 740	
tca gtt att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat	2308
Ser Val Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn	
745 750 755 760	
gaa ccc gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg	2356
Glu Pro Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg	
765 770 775	
ctt ttc act gaa aga ttg cac aag agt gac ctt gga ggg gtt tgg tgg	2404
Leu Phe Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp	
780 785 790	
tct tgc aaa ctg tac ata ccc aag gag gcc tac aga tta gac ttt gtg	2452

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Ser	Cys	Lys	Leu	Tyr	Ile	Pro	Lys	Glu	Ala	Tyr	Arg	Leu	Asp	Phe	Val	
		795					800					805				
ttc	ttc	aac	ggt	cgc	acg	gtc	tat	gag	aac	aat	ggc	aac	aat	gat	ttc	2500
Phe	Phe	Asn	Gly	Arg	Thr	Val	Tyr	Glu	Asn	Asn	Gly	Asn	Asn	Asp	Phe	
		810				815					820					
tgt	ata	gga	ata	gaa	ggc	act	atg	aat	gaa	gat	ctg	ttt	gag	gat	ttc	2548
Cys	Ile	Gly	Ile	Glu	Gly	Thr	Met	Asn	Glu	Asp	Leu	Phe	Glu	Asp	Phe	
		825				830				835					840	
ttg	gtt	aaa	gaa	aag	caa	agg	gag	ctt	gag	aaa	ctt	gcc	atg	gaa	gaa	2596
Leu	Val	Lys	Glu	Lys	Gln	Arg	Glu	Leu	Glu	Lys	Leu	Ala	Met	Glu	Glu	
				845					850					855		
gct	gaa	agg	agg	aca	cag	act	gaa	gaa	cag	cgg	cga	aga	aag	gaa	gca	2644
Ala	Glu	Arg	Arg	Thr	Gln	Thr	Glu	Glu	Gln	Arg	Arg	Arg	Lys	Glu	Ala	
			860					865					870			
agg	gct	gca	gat	gaa	gct	gtc	agg	gca	caa	gcg	aag	gcc	gag	ata	gag	2692
Arg	Ala	Ala	Asp	Glu	Ala	Val	Arg	Ala	Gln	Ala	Lys	Ala	Glu	Ile	Glu	
		875					880					885				
atc	aag	aag	aaa	aaa	ttg	caa	agt	atg	ttg	agt	ttg	gcc	aga	aca	tgt	2740
Ile	Lys	Lys	Lys	Lys	Leu	Gln	Ser	Met	Leu	Ser	Leu	Ala	Arg	Thr	Cys	
		890				895					900					
gtt	gat	aat	ttg	tgg	tac	ata	gag	gct	agc	aca	gat	aca	aga	gga	gat	2788
Val	Asp	Asn	Leu	Trp	Tyr	Ile	Glu	Ala	Ser	Thr	Asp	Thr	Arg	Gly	Asp	
					910					915					920	
act	atc	agg	tta	tat	tat	aac	aga	aac	tcg	agg	cca	ctt	gcg	cat	agt	2836
Thr	Ile	Arg	Leu	Tyr	Tyr	Asn	Arg	Asn	Ser	Arg	Pro	Leu	Ala	His	Ser	
				925					930					935		
act	gag	att	tgg	atg	cat	ggt	ggt	tac	aac	aat	tgg	aca	gat	gga	ctc	2884
Thr	Glu	Ile	Trp	Met	His	Gly	Gly	Tyr	Asn	Asn	Trp	Thr	Asp	Gly	Leu	
			940					945					950			
tct	att	gtt	gaa	agc	ttt	gtc	aag	tgc	aat	gac	aaa	gac	ggc	gat	tgg	2932
Ser	Ile	Val	Glu	Ser	Phe	Val	Lys	Cys	Asn	Asp	Lys	Asp	Gly	Asp	Trp	
		955					960					965				
tgg	tat	gca	gat	gtt	att	cca	cct	gaa	aag	gca	ctt	gtg	ttg	gac	tgg	2980
Trp	Tyr	Ala	Asp	Val	Ile	Pro	Pro	Glu	Lys	Ala	Leu	Val	Leu	Asp	Trp	
		970				975					980					
gtt	ttt	gct	gat	ggg	cca	gct	ggg	aat	gca	agg	aac	tat	gac	aac	aat	3028
Val	Phe	Ala	Asp	Gly	Pro	Ala	Gly	Asn	Ala	Arg	Asn	Tyr	Asp	Asn	Asn	
					990					995					1000	
gct	cga	caa	gat	ttc	cat	gct	att	ctt	ccg	aac	aac	aat	gta	acc	gag	3076
Ala	Arg	Gln	Asp	Phe	His	Ala	Ile	Leu	Pro	Asn	Asn	Asn	Val	Thr	Glu	
				1005					1010					1015		
gaa	ggc	ttc	tgg	gcg	caa	gag	gag	caa	aac	atc	tat	aca	agg	ctt	ctg	3124
Glu	Gly	Phe	Trp	Ala	Gln	Glu	Glu	Gln	Asn	Ile	Tyr	Thr	Arg	Leu	Leu	
			1020					1025					1030			
caa	gaa	agg	aga	gaa	aag	gaa	gaa	acc	atg	aaa	aga	aag	gct	gag	aga	3172
Gln	Glu	Arg	Arg	Glu	Lys	Glu	Glu	Thr	Met	Lys	Arg	Lys	Ala	Glu	Arg	
		1035					1040					1045				
agt	gca	aat	atc	aaa	gct	gag	atg	aag	gca	aaa	act	atg	cga	agg	ttt	3220
Ser	Ala	Asn	Ile	Lys	Ala	Glu	Met	Lys	Ala	Lys	Thr	Met	Arg	Arg	Phe	

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1050	1055	1060	
ctg ctt tcc cag aaa cac att gtt tat acc gaa ccg ctt gaa ata cgt			3268
Leu Leu Ser Gln Lys His Ile Val Tyr Thr Glu Pro Leu Glu Ile Arg			
1065	1070	1075	1080
gcc gga acc aca gtg gat gtg cta tac aat ccc tct aac aca gtg cta			3316
Ala Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu			
	1085	1090	1095
aat gga aag tcg gag ggt tgg ttt aga tgc tcc ttt aac ctt tgg atg			3364
Asn Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met			
	1100	1105	1110
cat tca agt ggg gca ttg cca ccc cag aag atg gtg aaa tca ggg gat			3412
His Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp			
	1115	1120	1125
ggg ccg ctc tta aaa gca aca gtt gat gtt cca ccg gat gcc tat atg			3460
Gly Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met			
	1130	1135	1140
atg gac ttt gtt ttc tcc gag tgg gaa gaa gat ggg atc tat gac aac			3508
Met Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn			
	1145	1150	1155
agg aat ggg atg gac tat cat att cct gtt tct gat tca att gaa aca			3556
Arg Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr			
	1165	1170	1175
gag aat tac atg cgt att atc cac att gcc gtt gag atg gcc ccc gtt			3604
Glu Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val			
	1180	1185	1190
gca aag gtt gga ggt ctt ggg gat gtt gtt aca agt ctt tca cgt gcc			3652
Ala Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala			
	1195	1200	1205
att caa gat cta gga cat act gtc gag gtt att ctc ccg aag tac gac			3700
Ile Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp			
	1210	1215	1220
tgt ttg aac caa agc agt gtc aag gat tta cat tta tat caa agt ttt			3748
Cys Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe			
	1225	1230	1235
tct tgg ggt ggt aca gaa ata aaa gta tgg gtt gga cga gtc gaa gac			3796
Ser Trp Gly Gly Thr Glu Ile Lys Val Trp Val Gly Arg Val Glu Asp			
	1245	1250	1255
ctg acc gtt tac ttc ctg gaa cct caa aat ggg atg ttt ggc gtt gga			3844
Leu Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly			
	1260	1265	1270
tgt gta tat gga agg aat gat gac cgc aga ttt ggg ttc ttc tgt cat			3892
Cys Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His			
	1275	1280	1285
tct gct cta gag ttt atc ctc cag aat gaa ttt tct cca cat ata ata			3940
Ser Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile			
	1290	1295	1300
cat tgc cat gat tgg tca agt gct ccg gtc gcc tgg cta tat aag gaa			3988
His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu			
	1305	1310	1315
			1320

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cac tat tcc caa tcc aga atg gca agc act cgg gtt gta ttt acc atc His Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile 1325 1330 1335	4036
cac aat ctt gaa ttt gga gca cat tat att ggt aaa gca atg aca tac His Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr 1340 1345 1350	4084
tgt gat aaa gcc aca act gtt tct cct aca tat tca agg gac gtg gca Cys Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala 1355 1360 1365	4132
ggc cat ggc gcc att gct cct cat cgt gag aaa ttc tac ggc att ctc Gly His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu 1370 1375 1380	4180
aat gga att gat cca gat atc tgg gat ccg tac act gac aat ttt atc Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile 1385 1390 1395 1400	4228
ccg gtc cct tat act tgt gag aat gtt gtc gaa ggc aag aga gct gca Pro Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala 1405 1410 1415	4276
aaa agg gcc ttg cag cag aag ttt gga tta cag caa act gat gtc cct Lys Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro 1420 1425 1430	4324
att gtc gga atc atc acc cgt ctg aca gcc cag aag gga atc cac ctc Ile Val Gly Ile Ile Thr Arg Leu Thr Ala Gln Lys Gly Ile His Leu 1435 1440 1445	4372
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ttg gcc gat gct ctt cat ggt gtt tac cat ggt agg gtg aag ctt gtt Leu Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val 1485 1490 1495	4516
cta acc tat gat gag cct ctt tct cac ctg ata tac gct ggc tcg gac Leu Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp 1500 1505 1510	4564
ttc ata att gtt cct tca atc ttc gaa ccc tgt ggc tta aca caa ctt Phe Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu 1515 1520 1525	4612
gtt gcc atg cgt tat gga tcg atc cct ata gtt cgg aaa act gga gga Val Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly 1530 1535 1540	4660
ctt cac gac aca gtc ttc gac gta gac aat gat aag gac cgg gct cgg Leu His Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg 1545 1550 1555 1560	4708
tct ctt ggt ctt gaa cca aat ggg ttc agt ttc gac gga gcc gac agc Ser Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser 1565 1570 1575	4756

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aat ggc gtg gat tat gcc ctc aac aga gca atc ggc gct tgg ttc gat 4804
 Asn Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp
 1580 1585 1590

gcc cgt gat tgg ttc cac tcc ctg tgt aag agg gtc atg gag caa gac 4852
 Ala Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp
 1595 1600 1605

tgg tcg tgg aac cgg ccc gca ctg gac tac att gaa ttg tac cat gcc 4900
 Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala
 1610 1615 1620

gct cga aaa ttc tgacacccaa ctgaaccaat gacaagaaca agcgcatgtg 4952
 Ala Arg Lys Phe
 1625

gggatcgact agtcatacag ggctgtgcag atcgtcttgc ttcagttagt gccctcttca 5012

gttagttcca agcgactac agtcgtacat agctgaggat cctcttgcct cctaccaggg 5072

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atgttaggct gtctgatcat gtggaagctt tggtatatgt tacttatggt atacatcaat 5312

gatatttaca tttgtggaaa aaaaaaaaaa aaaa 5346

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<211> 1628

<212> PRT

<213> Triticum aestivum

<400> 8

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Gln Pro Leu Val Val Val Arg Pro Ala Gly Arg Gly Gly Leu Thr Gln
 20 25 30

Pro Phe Leu Met Asn Gly Arg Phe Thr Arg Ser Arg Thr Leu Arg Cys
 35 40 45

Met Val Ala Ser Ser Asp Pro Pro Asn Arg Lys Ser Arg Arg Met Val
 50 55 60

Pro Pro Gln Val Lys Val Ile Ser Ser Arg Gly Tyr Thr Thr Arg Leu
 65 70 75 80

Ile Val Glu Pro Ser Asn Glu Asn Thr Glu His Asn Asn Arg Asp Glu
 85 90 95

Glu Thr Leu Asp Thr Tyr Asn Ala Leu Leu Ser Thr Glu Thr Ala Glu
 100 105 110

Trp Thr Asp Asn Arg Glu Ala Glu Thr Ala Lys Ala Asp Ser Ser Gln
 115 120 125

Asn Ala Leu Ser Ser Ser Ile Ile Gly Glu Val Asp Val Ala Asp Glu
 130 135 140

Asp Ile Leu Ala Ala Asp Leu Thr Val Tyr Ser Leu Ser Ser Val Met

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145		150		155		160
Lys Lys Glu Val Asp	Ala Ala Asp Lys	Ala Arg Val Lys	Glu Asp Ala			
	165	170	175			
Phe Glu Leu Asp Leu	Pro Ala Thr Thr	Leu Arg Ser Val	Ile Val Asp			
	180	185	190			
Val Met Asp His Asn	Gly Thr Val Gln	Glu Thr Leu Arg	Ser Val Ile			
	195	200	205			
Val Asp Val Met Asp	His Asn Gly Thr	Val Gln Glu Thr	Leu Arg Ser			
	210	215	220			
Val Ile Val Asp Val	Met Asp Asp Ala	Ala Asp Lys Ala	Arg Val Glu			
	225	230	235			240
Glu Asp Val Phe Glu	Leu Asp Leu Ser	Gly Asn Ile Ser	Ser Ser Ser	Ala		
	245	250	255			
Thr Thr Val Glu Leu	Asp Ala Val Asp	Glu Val Gly Pro	Val Gln Asp			
	260	265	270			
Lys Phe Glu Ala Thr	Ser Ser Gly Asn	Val Ser Asn Ser	Ala Thr Val			
	275	280	285			
Arg Glu Val Asp Ala	Ser Asp Glu Ala	Gly Asn Asp Gln	Gly Ile Phe			
	290	295	300			
Arg Ala Asp Leu Ser	Gly Asn Val Phe	Ser Ser Ser Thr	Thr Val Glu			
	305	310	315			320
Val Gly Ala Val Asp	Glu Ala Gly Ser	Ile Lys Asp Arg	Phe Glu Thr			
	325	330	335			
Asp Ser Ser Gly Asn	Val Ser Thr Ser	Ala Pro Met Trp	Asp Ala Ile			
	340	345	350			
Asp Glu Thr Val Ala	Asp Gln Asp Thr	Phe Glu Ala Asp	Leu Ser Gly			
	355	360	365			
Asn Ala Ser Ser Cys	Ala Thr Tyr Arg	Glu Val Asp Asp	Val Val Asp			
	370	375	380			
Glu Thr Arg Ser Glu	Glu Glu Thr Phe	Ala Met Asp Leu	Phe Ala Ser			
	385	390	395			400
Glu Ser Gly His Glu	Lys His Met Ala	Val Asp Tyr Val	Gly Glu Ala			
	405	410	415			
Thr Asp Glu Glu Glu	Thr Tyr Gln Gln	Gln Tyr Pro Val	Pro Ser Ser			
	420	425	430			
Phe Ser Met Trp Asp	Lys Ala Ile Ala	Lys Thr Gly Val	Ser Leu Asn			
	435	440	445			
Pro Glu Leu Arg Leu	Val Arg Val Glu	Glu Gln Gly Lys	Val Asn Phe			
	450	455	460			
Ser Asp Lys Lys Asp	Leu Ser Ile Asp	Asp Leu Pro Gly	Gln Asn Gln			
	465	470	475			480
Ser Ile Ile Gly Ser	Tyr Lys Gln Asp	Lys Ser Ile Ala	Asp Val Ala			
	485	490	495			

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Gly Pro Thr Gln Ser Ile Phe Gly Ser Ser Lys Gln His Arg Ser Ile
 500 505 510
 Val Ala Phe Pro Lys Gln Asn Gln Ser Ile Val Ser Val Thr Glu Gln
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 Lys Gln Ser Ile Val Gly Phe Arg Ser Gln Asp Leu Ser Ala Val Ser
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 Leu Pro Lys Gln Asn Val Pro Ile Val Gly Thr Ser Arg Glu Gly Gln
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 Asp Ala Leu His Val Lys Phe Asn Val Asp Asn Val Leu Arg Lys His
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 Asp Glu Glu His Leu Tyr Met Thr Glu His Gln Lys Arg Ala Ala Glu
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 645 650 655
 Met Gly Arg Gly Asp Lys Ile Gln His Val Leu Ser Glu Glu Glu Leu
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 Ser Trp Ser Glu Asp Glu Val Gln Leu Ile Glu Asp Asp Gly Gln Tyr
 675 680 685
 Glu Val Asp Glu Thr Ser Val Ser Val Asn Val Glu Gln Asp Ile Gln
 690 695 700
 Gly Ser Pro Gln Asp Val Val Asp Pro Gln Ala Leu Lys Val Met Leu
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 Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met Arg Asn Lys Leu Phe Val
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 Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro Asp Val Val Ile Lys Gly
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 Ser Asp Leu Gly Gly Val Trp Trp Ser Cys Lys Leu Tyr Ile Pro Lys
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 Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe Asn Gly Arg Thr Val Tyr
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 Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile Gly Ile Glu Gly Thr Met
 820 825 830
 Asn Glu Asp Leu Phe Glu Asp Phe Leu Val Lys Glu Lys Gln Arg Glu
 835 840 845

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Leu Glu Lys Leu Ala Met Glu Glu Ala Glu Arg Arg Thr Gln Thr Glu
 850 855 860
 Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala Ala Asp Glu Ala Val Arg
 865 870 875 880
 Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys Lys Lys Lys Leu Gln Ser
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 Met Leu Ser Leu Ala Arg Thr Cys Val Asp Asn Leu Trp Tyr Ile Glu
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 Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile Arg Leu Tyr Tyr Asn Arg
 915 920 925
 Asn Ser Arg Pro Leu Ala His Ser Thr Glu Ile Trp Met His Gly Gly
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 Tyr Asn Asn Trp Thr Asp Gly Leu Ser Ile Val Glu Ser Phe Val Lys
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 Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr Ala Asp Val Ile Pro Pro
 965 970 975
 Glu Lys Ala Leu Val Leu Asp Trp Val Phe Ala Asp Gly Pro Ala Gly
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 995 1000 1005
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 Pro Val Ser Asp Ser Ile Glu Thr Glu Asn Tyr Met Arg Ile Ile His
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 Ile Ala Val Glu Met Ala Pro Val Ala Lys Val Gly Gly Leu Gly Asp

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 Asp Leu His Leu Tyr Gln Ser Phe Ser Trp Gly Gly Thr Glu Ile Lys
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 Ser Thr Arg Val Val Phe Thr Ile His Asn Leu Glu Phe Gly Ala His
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 Pro Thr Tyr Ser Arg Asp Val Ala Gly His Gly Ala Ile Ala Pro His
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 Val Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe
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 Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His Arg Thr
 1445 1450 1455
 Leu Glu Ser Asn Gly His Val Val Leu Leu Gly Ser Ala Pro Asp His
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 Arg Ile Gln Gly Asp Phe Cys Arg Leu Ala Asp Ala Leu His Gly Val
 1475 1480 1485
 Tyr His Gly Arg Val Lys Leu Val Leu Thr Tyr Asp Glu Pro Leu Ser
 1490 1495 1500
 His Leu Ile Tyr Ala Gly Ser Asp Phe Ile Ile Val Pro Ser Ile Phe
 505 1510 1515 1520
 Glu Pro Cys Gly Leu Thr Gln Leu Val Ala Met Arg Tyr Gly Ser Ile
 1525 1530 1535

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Pro Ile Val Arg Lys Thr Gly Gly Leu His Asp Thr Val Phe Asp Val
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Asp Asn Asp Lys Asp Arg Ala Arg Ser Leu Gly Leu Glu Pro Asn Gly
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Phe Ser Phe Asp Gly Ala Asp Ser Asn Gly Val Asp Tyr Ala Leu Asn
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Arg Ala Ile Gly Ala Trp Phe Asp Ala Arg Asp Trp Phe His Ser Leu
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 Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn Val Asp
 20 25 30

aat gtg ttg cgg aag cat cag gca gat aga acc caa gca gtg gaa aag 144
 Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val Glu Lys
 35 40 45

aaa act tgg aag aaa gtt gat gag gaa cat ctt tac atg act gaa cat 192
 Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr Glu His
 50 55 60

cag aaa cgt gct gcc gaa gga cag atg gta gtt aac gag gat gag ctt 240
 Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp Glu Leu
 65 70 75 80

tct ata act gaa att gga atg ggg aga ggt gat aaa att cag cat gtg 288
 Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln His Val
 85 90 95

ctt tct gag gaa gag ctt tca tgg tct gaa gat gaa gtg cag tta att 336
 Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln Leu Ile
 100 105 110

gag gat gat gga caa tat gaa gtt gac gag acc tct gtg tcc gtt aac 384
 Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser Val Asn
 115 120 125

gtt gaa caa gat atc cag ggg tca cca cag gat gtt gtg gat ccg caa 432
 Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp Pro Gln
 130 135 140

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145 150 155 160	
agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat tca gtt	528
Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp Ser Val	
165 170 175	
att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat gaa ccc	576
Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro	
180 185 190	
gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg ctt ttc	624
Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe	
195 200 205	
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Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp Ser Cys	
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Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe	
225 230 235 240	
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Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile	
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Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe Leu Val	
260 265 270	
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Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu Ala Glu	
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Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala	
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Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys	
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aag aaa aaa ttg caa agt atg ttg agt ttg gcc aga aca tgt gtt gat	1008
Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp	
325 330 335	
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Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile	
340 345 350	
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Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu	
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Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile	
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gtt gaa agc ttt gtc aag tgc aat gac aaa gac ggc gat tgg tgg tat	1200
Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr	
385 390 395 400	
gca gat gtt att cca cct gaa aag gca ctt gtg ttg gac tgg gtt ttt	1248

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Ala Asp Val Ile Pro Pro Glu Lys Ala Leu Val Leu Asp Trp Val Phe	
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gct gat ggg cca gct ggg aat gca agg aac tat gac aac aat gct cga	1296
Ala Asp Gly Pro Ala Gly Asn Ala Arg Asn Tyr Asp Asn Ala Arg	
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caa gat ttc cat gct att ctt ccg aac aac aat gta acc gag gaa ggc	1344
Gln Asp Phe His Ala Ile Leu Pro Asn Asn Asn Val Thr Glu Glu Gly	
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Phe Trp Ala Gln Glu Glu Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu	
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Arg Arg Glu Lys Glu Glu Thr Met Lys Arg Lys Ala Glu Arg Ser Ala	
465 470 475 480	
aat atc aaa gct gag atg aag gca aaa act atg cga agg ttt ctg ctt	1488
Asn Ile Lys Ala Glu Met Lys Ala Lys Thr Met Arg Arg Phe Leu Leu	
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tcc cag aaa cac att gtt tat acc cga acc gnc ttg aaa tac gtg ccc	1536
Ser Gln Lys His Ile Val Tyr Thr Arg Thr Xaa Leu Lys Tyr Val Pro	
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Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met Met	
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Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn Arg	
580 585 590	
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Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr Glu	
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Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val Ala	
610 615 620	
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Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Ile	
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Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp Cys	
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Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe Ser	

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acc gtt tac ttc ctg gaa cct caa aat ggg atg ttt ggc gtt gga tgt Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Cys 690 695 700			2112
gta tat gga agg aat gat gac cgc aga ttt ggg ttc ttc tgt cat tct Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His Ser 705 710 715 720			2160
gct cta gag ttt atc ctc cag aat gaa ttt tct cca cat ata ata cat Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile His 725 730 735			2208
tgc cat gat tgg tca agt gct ccg gtc gcc tgg cta tat aag gaa cac Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu His 740 745 750			2256
tat tcc caa tcc aga atg gca agc act cgg gtt gta ttt acc atc cac Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile His 755 760 765			2304
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gat aaa gcc aca act gtt tct cct aca tat tca agg gac gtg gca ggc Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala Gly 785 790 795 800			2400
cat ggc gcc att gct cct cat cgt gag aaa ttc tac ggc att ctc aat His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu Asn 805 810 815			2448
gga att gat cca gat atc tgg gat ccg tac act gac aat ttt atc ccg Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile Pro 820 825 830			2496
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ctt ggt tca gct cca gat cat cga ata caa ggc gat ttt tgc aga ttg Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg Leu 900 905 910			2736
gcc gat gct ctt cac ggt gtt tac cat ggt agg gtg aag ctt gtt cta Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val Leu 915 920 925			2784

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acc tac gat gag cct ctt tct cac ctg ata tac gct ggc tcc gac ttc 2832
Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe
    930                      935                      940

att att gtc cct tca atc ttt gaa ccc tgt ggc tta aca caa ctt gtt 2880
Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
    945                      950                      955                      960

gcc atg cgt tat gga tcg atc cct ata gtt cgg aaa acc gga gga ctt 2928
Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly Leu
                      965                      970                      975

tac gac act gtc ttc gac gta gac aat gat aag gac cgg gct cgg tct 2976
Tyr Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg Ser
                      980                      985                      990

ctt ggt ctt gaa cca aat ggg ttc agt ttc gac gga gcc gac agc aat 3024
Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser Asn
    995                      1000                      1005

ggc gtg gat tat gcc ctc aac aga gca atc ggc gct tgg ttc gat gcc 3072
Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp Ala
    1010                      1015                      1020

cgt gat tgg ttc cac tcc ctg tgt aag agg gtc atg gag caa gac tgg 3120
Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp Trp
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tcg tgg aac cgg cct gca ctg gac tac att gaa ttg tac cat gcc gct 3168
Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala Ala
                      1045                      1050                      1055

cga aaa ttc tgacacccaa ctgaaccaat ggcaagaaca agcgcattgt 3217
Arg Lys Phe

gggatcgact acagtcatac agggctgtgc agatcgtctt gcttcagtta gtgccctctt 3277

cagttagttc caagcgcaact acagtcgtac atagctgagg atcctcttgc ctcctccacc 3337

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Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val Glu Lys
    35          40          45

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Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr Glu His
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 65 70 75 80
 Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln His Val
 85 90 95
 Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln Leu Ile
 100 105 110
 Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser Val Asn
 115 120 125
 Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp Pro Gln
 130 135 140
 Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met
 145 150 155 160
 Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp Ser Val
 165 170 175
 Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro
 180 185 190
 Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe
 195 200 205
 Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp Ser Cys
 210 215 220
 Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe
 225 230 235 240
 Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile
 245 250 255
 Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe Leu Val
 260 265 270
 Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu Ala Glu
 275 280 285
 Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala
 290 295 300
 Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys
 305 310 315 320
 Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp
 325 330 335
 Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile
 340 345 350
 Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu
 355 360 365
 Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile
 370 375 380
 Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr

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385		390		395		400
Ala Asp Val Ile	Pro Pro Glu Lys	Ala Leu Val Leu	Asp Trp Val Phe			
	405	410	415			
Ala Asp Gly Pro	Ala Gly Asn Ala	Arg Asn Tyr Asp	Asn Asn Ala Arg			
	420	425	430			
Gln Asp Phe His	Ala Ile Leu Pro	Asn Asn Asn Val	Thr Glu Glu Gly			
	435	440	445			
Phe Trp Ala Gln	Glu Glu Gln Asn	Ile Tyr Thr Arg	Leu Leu Gln Glu			
	450	455	460			
Arg Arg Glu Lys	Glu Glu Thr Met	Lys Arg Lys Ala	Glu Arg Ser Ala			
	465	470	475	480		
Asn Ile Lys Ala	Glu Met Lys Ala	Lys Thr Met Arg	Arg Phe Leu Leu			
	485	490	495			
Ser Gln Lys His	Ile Val Tyr Thr	Arg Thr Xaa Leu	Lys Tyr Val Pro			
	500	505	510			
Gly Thr Thr Val	Asp Val Leu Tyr	Asn Pro Ser Asn	Thr Val Leu Asn			
	515	520	525			
Gly Lys Ser Glu	Gly Trp Phe Arg	Cys Ser Phe Asn	Leu Trp Met His			
	530	535	540			
Ser Ser Gly Ala	Leu Pro Pro Gln	Lys Met Val Lys	Ser Gly Asp Gly			
	545	550	555	560		
Pro Leu Leu Lys	Ala Thr Val Asp	Val Pro Pro Asp	Ala Tyr Met Met			
	565	570	575			
Asp Phe Val Phe	Ser Glu Trp Glu	Glu Asp Gly Ile	Tyr Asp Asn Arg			
	580	585	590			
Asn Gly Met Asp	Tyr His Ile Pro	Val Ser Asp Ser	Ile Glu Thr Glu			
	595	600	605			
Asn Tyr Met Arg	Ile Ile His Ile	Ala Val Glu Met	Ala Pro Val Ala			
	610	615	620			
Lys Val Gly Gly	Leu Gly Asp Val	Val Thr Ser Leu	Ser Arg Ala Ile			
	625	630	635	640		
Gln Asp Leu Gly	His Thr Val Glu	Val Ile Leu Pro	Lys Tyr Asp Cys			
	645	650	655			
Leu Asn Gln Ser	Ser Val Lys Asp	Leu His Leu Tyr	Gln Ser Phe Ser			
	660	665	670			
Trp Gly Gly Thr	Glu Ile Lys Val	Trp Val Gly Arg	Val Glu Asp Leu			
	675	680	685			
Thr Val Tyr Phe	Leu Glu Pro Gln	Asn Gly Met Phe	Gly Val Gly Cys			
	690	695	700			
Val Tyr Gly Arg	Asn Asp Asp Arg	Arg Phe Gly Phe	Phe Cys His Ser			
	705	710	715	720		
Ala Leu Glu Phe	Ile Leu Gln Asn	Glu Phe Ser Pro	His Ile Ile His			
	725	730	735			

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Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu His
 740 745 750
 Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile His
 755 760 765
 Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr Cys
 770 775 780
 Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala Gly
 785 790 795 800
 His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu Asn
 805 810 815
 Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile Pro
 820 825 830
 Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala Lys
 835 840 845
 Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro Ile
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 Lys His Ala Ile His Arg Thr Leu Glu Ser Asn Gly Gln Val Val Leu
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 Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg Leu
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 Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val Leu
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<211> 728

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<212> DNA

<213> *Triticum* sp.

<400> 11

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<210> 12

<211> 2446

<212> DNA

<213> *Triticum* sp.

<400> 12

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<211> 1032

<212> DNA

<213> *Triticum* sp.

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<210> 14

<211> 892

<212> DNA

<213> Triticum sp.

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- 40 -

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<210> 15
 <211> 871
 <212> DNA
 <213> Triticum sp.

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 <211> 1592
 <212> DNA
 <213> Triticum sp.

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<212> PRT

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<220>

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<210> 18

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 18

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 1 5 10

<210> 19

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<211> 10
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<220>
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<400> 19
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<210> 20
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<210> 21
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<220>
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<400> 21
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<210> 22
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<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 22
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<210> 23
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 23
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<210> 24
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

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<210> 25
<211> 23
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<220>
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<210> 26
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence:PRIMER

<400> 26
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<210> 27
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<220>
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<400> 27
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<210> 28
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<400> 28
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<210> 29
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<220>
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<400> 29
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<210> 30
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<210> 31
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<223> Description of Artificial Sequence:PRIMER

<400> 31
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<210> 32
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<400> 32
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<210> 33
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<400> 33
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<210> 34
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<220>
<223> Description of Artificial Sequence:PRIMER

<400> 34

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<210> 35

<211> 25

<212> PRT

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<220>

<223> Description of Artificial Sequence:PEPTIDE MOTIF

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Gln	Asp	Leu	Gly	His	Asn	Val	Glu	Val
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<210> 36

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 36

Lys	Val	Gly	Gly	Leu	Gly	Asp	Val	Val	Thr	Ser	Leu	Ser	Arg	Ala	Ile
1				5					10					15	

Gln	Asp	Leu	Gly	His	Thr	Val	Glu	Val
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<210> 37

<211> 9024

<212> DNA

<213> Triticum sp.

<400> 37

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- 54 -

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PATENT COOPERATION TREATY
PCT
INTERNATIONAL PRELIMINARY EXAMINATION

REC'D 10 APR 2001

REPORT

PCT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 2288545/MRO/wm	FOR FURTHER ACTION	See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416).
International Application No. PCT/AU00/00385	International Filing Date (<i>day/month/year</i>) 28 April 2000	Priority Date (<i>day/month/year</i>) 29 April 1999
International Patent Classification (IPC) or national classification and IPC Int. Cl.⁷ C12N 15/54; A01H 1/00, 5/00; C08B 3/02; C12N 9/10, 15/11; C12Q 1/48, 1/68		
Applicant COMMONWEALTH SCIENTIFIC & INDUSTRIAL RESEARCH ORGANISATION et al		

1.	This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.																
2.	This REPORT consists of a total of 4 sheets, including this cover sheet. <input type="checkbox"/> This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT). These annexes consist of a total of sheet(s).																
3.	This report contains indications relating to the following items: <table border="0"><tr><td>I</td><td><input checked="" type="checkbox"/> Basis of the report</td></tr><tr><td>II</td><td><input type="checkbox"/> Priority</td></tr><tr><td>III</td><td><input type="checkbox"/> Non-establishment of opinion with regard to novelty, inventive step and industrial applicability</td></tr><tr><td>IV</td><td><input type="checkbox"/> Lack of unity of invention</td></tr><tr><td>V</td><td><input checked="" type="checkbox"/> Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement</td></tr><tr><td>VI</td><td><input checked="" type="checkbox"/> Certain documents cited</td></tr><tr><td>VII</td><td><input type="checkbox"/> Certain defects in the international application</td></tr><tr><td>VIII</td><td><input type="checkbox"/> Certain observations on the international application</td></tr></table>	I	<input checked="" type="checkbox"/> Basis of the report	II	<input type="checkbox"/> Priority	III	<input type="checkbox"/> Non-establishment of opinion with regard to novelty, inventive step and industrial applicability	IV	<input type="checkbox"/> Lack of unity of invention	V	<input checked="" type="checkbox"/> Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement	VI	<input checked="" type="checkbox"/> Certain documents cited	VII	<input type="checkbox"/> Certain defects in the international application	VIII	<input type="checkbox"/> Certain observations on the international application
I	<input checked="" type="checkbox"/> Basis of the report																
II	<input type="checkbox"/> Priority																
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V	<input checked="" type="checkbox"/> Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement																
VI	<input checked="" type="checkbox"/> Certain documents cited																
VII	<input type="checkbox"/> Certain defects in the international application																
VIII	<input type="checkbox"/> Certain observations on the international application																

Date of submission of the demand 31 October 2000	Date of completion of the report 30 March 2001
Name and mailing address of the IPEA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaaustralia.gov.au Facsimile No. (02) 6285 3929	Authorized Officer GARETH COOK Telephone No. (02) 6283 2541

I. Basis of the report

1. With regard to the elements of the international application:*
- ☒ the international application as originally filed.
- ☐ the description, pages , as originally filed,
 pages , filed with the demand,
 pages , received on with the letter of
- ☐ the claims, pages , as originally filed,
 pages , as amended (together with any statement) under Article 19,
 pages , filed with the demand,
 pages , received on with the letter of
- ☐ the drawings, pages , as originally filed,
 pages , filed with the demand,
 pages , received on with the letter of
- ☐ the sequence listing part of the description:
 pages , as originally filed
 pages , filed with the demand
 pages , received on with the letter of
2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.
 These elements were available or furnished to this Authority in the following language which is:
- ☐ the language of a translation furnished for the purposes of international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of the translation furnished for the purposes of international preliminary examination (under Rules 55.2 and/or 55.3).
3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, was on the basis of the sequence listing:
- ☒ contained in the international application in written form.
- ☒ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished
4. ☐ The amendments have resulted in the cancellation of:
- ☐ the description, pages
- ☐ the claims, Nos.
- ☐ the drawings, sheets/fig.
5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).**

* Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17).

** Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement**1. Statement**

Novelty (N)	Claims 9, 20, 39 and 40	YES
	Claims 1-8, 10-19, 21-38 and 41-59	NO
Inventive step (IS)	Claims 9, 20, 39 and 40	YES
	Claims 1-8, 10-19, 21-38 and 41-59	NO
Industrial applicability (IA)	Claims 1-59	YES
	Claims	NO

2. Citations and explanations (Rule 70.7)

The following documents identified in the International Search Report have been considered for the purposes of this report:

- D3 WO 97/45545 (HOECHST SCHERING AGREVO GmbH)
- D4 Walter L *et al*, (a) GenPept Accession AAB17085 and (b) GenBank accession U66377
- D5 Gao M *et al*, GenPept accession AAC14014
- D6 GenPept accession AAC14015
- D7 D'Hulst C *et al*, GenPept accession AAC17969
- D8 Bullar SS *et al*, GenPept accession CAB40374

Novelty (N) and Inventive Step (IS) claims 1-8, 10-19, 21-38 and 41-59

Document D3 discloses sequences (SEQ ID NO: 5) which fall within the condition of 85% identity to SEQ ID NO's 1-6, 50 and 53. The document also teaches using these sequences which encode starch synthase, to transform plants. As such the invention as defined in claims 1-8, 10-19, 21-38 and 41-59 is not novel and lacks an inventive step under Article 33 of the PCT.

Documents D4(a) GenPept acc. no AAB17085 and D4(b) GenBank acc. no.U66377 disclose a peptide sequence for the wheat starch synthase and its encoding nucleotide sequence. These sequences falls within the criterion of 85% identity to the sequences defined in claims 1 and 12. As such the invention as defined in claims 1-8, 10-19 and 21 is not novel and lacks an inventive step under Article 33 of the PCT.

It would be obvious for a PSA to combine the information on the sequences in D4(a) or (b) with the teaching on the transformation of plants in D3 to transform plant using these sequences. As such the invention as defined in claims 21-38 and 41-59 lacks an inventive step under Article 33 of the PCT in the light of the combined teaching of D3 and D4.

Documents D5-D8 discloses sequences which contain the sequence defined in claim 18 (a)-(h): D5 discloses (a), (c) and (d); D6 discloses (c), (d) and (e); D7 discloses (f), and; D8 discloses (b). As such the invention as defined in claim 18 lacks novelty and does not involved an inventive step under Article 33 of the PCT.

Industrial applicability:

The invention as defined in claims 1-59 is useful in agriculture and food production, as such it has industrial applicability.

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.

PCT/AU00/00385

VI. Certain documents cited**1. Certain published documents (Rule 70.10)**Application No.
Patent No.Publication date
(day/month/year)Filing date
(day/month/year)Priority date (valid claim)
(day/month/year)

The inventors of the present application authored document D1 (Li Z *et al*, Plant Physiology, August 1999, 120(4):1147-1156) disclosing the same subject matter as the current application.

Documents D2(a) and D2(b) (Gao M *et al*, GenPept accession CAB86618 and GenBank accession AJ269502) disclose sequences which fall within the criterion of 85% identity to SEQ ID NO's 1-6, 50 and 53 of this application.

These documents are published after the priority date of the present application.

2. Non-written disclosures (Rule 70.9)

Kind of non-written disclosure

Date of non-written disclosure
(day/month/year)Date of written disclosure referring to non-
written disclosure
(day/month/year)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU00/00385

A. CLASSIFICATION OF SUBJECT MATTERInt. Cl. ⁷: C12N 15/54, 15/11; C12N 9/10; C12Q 1/48, 1/68; A01H 1/00, 5/00; C08B 3/02.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHEDMinimum documentation searched (classification system followed by classification symbols)
WORLD PATENT INDEX (WPI).Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
GENBANK, EMBL, SWISS-PROTEINS, PIRElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)
KW: WPI Starch synthase. Seq id nos 2, 4, 6, 8, 10 and 39-54.**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	Li Z <i>et al</i> "The localization and expression of the class II starch synthases of wheat" Plant Physiol 1999 Aug 120(4) pp 1147-1156. See the whole document.	1-59.
P, X	GenPept accession no. CAB86618, and GenBank accession no. AJ269502, published 7 April 2000. Gao M and Chibbar R N "Isolation, characterization and expression analysis of starch synthase IIa c DNA from wheat (<i>Triticum aestivum</i> L.)" See the whole document.	1-8, 10-19 and 21 (seq id nos 1-6, 50 and 53)
X; Y	WO 97/45545 A (HOECHST SCHERING AGREVO GmbH) 4 December 1997. See the whole document especially the examples and seq id no 5.	1-8, 10-19, 21-38 and 41-59 (seq id nos 1-6, 50 and 53)

☒ Further documents are listed in the continuation of Box C ☒ See patent family annex

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 16 June 2000	Date of mailing of the international search report 20 JUN 2000
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustalia.gov.au Facsimile No. (02) 6285 3929	Authorized officer J.H. CHAN Telephone No : (02) 6283 2340

International application No.
PCT/AU00/00385

Patent Document Cited in Search Report				Patent Family Member			
WO	9745545	AU	30302/97	BR	9709487	CN	1219970
		CZ	9803890	DE	19621588	EP	907741
		SK	1636/98	ZA	9704657		
END OF ANNEX							